STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number 177728

TO: James Schultz
Location: 2d18 / 2c18
Art Unit: 1635
Tuesday, February 07, 2006

Case Serial Number: 09/889075

From: Noble Jarrell
Location: Biotech-Chem Library
Rem 1B71
Phone: 272-2556

Noble.jarrell@uspto.gov

Search Notes

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 80.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

Minlen = 20

Maxlen = 50

177728

STIC-Biotech/ChemLib

From: Schultz, James
Sent: Thursday, January 26, 2006 2:14 PM
To: STIC-Biotech/ChemLib
Subject: Seq Search 09/889,075

Hello,
Could you please run a score over length nucleotide sequence search against nucleotides 168 to 332 of SEQ ID NO:1 in the above entitled application,

AND

a standard length limited nucleotide sequence search against SEQ ID NO: 6 in the same application...

No need for interference databases to be searched, and please return the results to me via email or diskette (i.e. a digital copy) and paper (for the IFW file).

I need both sequences searched because they are used together. Please let me know if I should run this through the sequence search approval folks.

Thanks much,
Doug Schultz

LRTE

James Douglas Schultz, PhD
Primary Examiner
AU 1635 (Biotechnology)
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

****
Searcher: noble
Searcher Phone:
Date Searcher Picked up: 2/7/06
Date completed:
Searcher Prep Time: 480
Online Time: 10

****
Type of Search
NA# 12 AA#:
S/L: x Oligomer:
Encode/Transl:
Structure #: Text:
Inventor: Litigation:

****
Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM: Compugen 909
WWW/Internet:
Other (Specify):

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 13:40:34 ; Search time 0.001 Seconds
(without alignments)
16.500 Million cell updates/sec

Title: US-09-889-075-1
Perfect score: 165
Sequence: 1 cgcatgtaacccggccaggc.....cagatctctgacccgttcgg 165

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 50 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : fetch1rni.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25	15.2	25	1	US-08-626-169-12	Sequence 12, Appl
2	25	15.2	25	1	US-09-164-907-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-626-169-12
; Sequence 12, Application US/08626169
; Patent No. 5861248
; GENERAL INFORMATION:
; APPLICANT: Russell, David W.
; APPLICANT: Thigpen, Anice E.
; TITLE OF INVENTION: BIOMARKERS FOR DETECTION, DIAGNOSIS
; TITLE OF INVENTION: AND PROGNOSIS OF PROSTATE CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/626,169
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Corder, Timothy S.
; REGISTRATION NUMBER: 38,414
; REFERENCE/DOCKET NUMBER: UROC:007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-626-169-12

Query Match 15.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        271 ATGGCCGCGGCCAAGGCCGAGATGC 295
              |||||||||||||||||||||||||
Db          1 ATGGCCGCGGCCAAGGCCGAGATGC 25
```

RESULT 2
US-09-164-907-12
; Sequence 12, Application US/09164907A
; Patent No. 6090559
; GENERAL INFORMATION:
; APPLICANT: RUSSELL, DAVID W.
; APPLICANT: THIGPEN, ANICE E.
; TITLE OF INVENTION: BIOMARKERS FOR DETECTION, DIAGNOSIS AND PROGNOSIS OF
; TITLE OF INVENTION: PROSTATE CANCER
; FILE REFERENCE: UROC:021
; CURRENT APPLICATION NUMBER: US/09/164,907A
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 08/626,169
; EARLIER FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-164-907-12

Query Match 15.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        271 ATGGCCGCGGCCAAGGCCGAGATGC 295
              |||||||||||||||||||||||||
Db          1 ATGGCCGCGGCCAAGGCCGAGATGC 25
```

Search completed: February 7, 2006, 13:40:35
Job time : 1 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 13:41:59 ; Search time 0.001 Seconds
(without alignments)
20.790 Million cell updates/sec

Title: US-09-889-075-1
Perfect score: 165
Sequence: 1 cgcatgtaacccggccaggc.....cagatctctgacccgttcgg 165

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 3 seqs, 63 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database : fetch1rnpbm.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	11.5	21	1	US-10-288-230-3	Sequence 3, Appli
2	19	11.5	21	1	US-10-892-527A-7	Sequence 7, Appli
c 3	19	11.5	21	1	US-10-892-527A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-288-230-3
; Sequence 3, Application US/10288230
; Publication No. US20030157030A1
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THERAPEUTIC USE OF RNA INTERFERENCE
; FILE REFERENCE: ITI-P01-001
; CURRENT APPLICATION NUMBER: US/10/288,230
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/336314
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for synthesis of siRNA directed against Egr-1
; OTHER INFORMATION: gene
US-10-288-230-3

Query Match 11.5%; Score 19; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 0.87;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy      262 TCGTCCAGGATGGCCGCGG 280
            :||:||||||:||||||||
Db        1 UCGUCCAGGAUGGCCGCGG 19
```

RESULT 2
US-10-892-527A-7
; Sequence 7, Application US/10892527A
; Publication No. US20050136430A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Mark E.
; TITLE OF INVENTION: INHIBITOR NUCLEIC ACIDS
; FILE REFERENCE: CTCH-P01-020
; CURRENT APPLICATION NUMBER: US/10/892,527A
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,570
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 60/528,143
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically synthesized
US-10-892-527A-7

Query Match 11.5%; Score 19; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 0.87;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy      262 TCGTCCAGGATGGCCGCGG 280
            :||:||||||:||||||||
Db        1 UCGUCCAGGAUGGCCGCGG 19
```

RESULT 3
US-10-892-527A-8/c
; Sequence 8, Application US/10892527A
; Publication No. US20050136430A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Mark E.
; TITLE OF INVENTION: INHIBITOR NUCLEIC ACIDS
; FILE REFERENCE: CTCH-P01-020
; CURRENT APPLICATION NUMBER: US/10/892,527A
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,570
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 60/528,143
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically synthesized
US-10-892-527A-8

Query Match 11.5%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      262 TCGTCCAGGATGGCCGCGG 280
            ||||||||||||||||||||
Db       19 TCGTCCAGGATGGCCGCGG 1
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 13:37:42 ; Search time 0.001 Seconds
(without alignments)
8.250 Million cell updates/sec

Title: US-09-889-075-1
Perfect score: 165
Sequence: 1 cgcatgtaacccggccaggc.....cagatctctgacccgttcgg 165

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 25 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : fetch1rge.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25	15.2	25	1	AR030267	ACCESSION:AR030267

ALIGNMENTS

RESULT 1
AR030267
LOCUS AR030267 25 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5861248.
ACCESSION AR030267
VERSION AR030267.1 GI:5943481
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Russell,D.W. and Thigpen,A.E.
TITLE Biomarkers for detection of prostate cancer
JOURNAL Patent: US 5861248-A 12 19-JAN-1999;
FEATURES Location/Qualifiers
source 1. .25
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 15.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        271 ATGGCCGCGGCCAAGGCCGAGATGC 295
              |||||||||||||||||||||||||
Db          1 ATGGCCGCGGCCAAGGCCGAGATGC 25
```

Search completed: February 7, 2006, 13:37:43
Job time : 0.001 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 13:38:54 ; Search time 0.001 Seconds
(without alignments)
56.760 Million cell updates/sec

Title: US-09-889-075-1
Perfect score: 165
Sequence: 1 cgcatgtaacccggccaggc.....cagatctctgacccgttcgg 165

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 8 seqs, 172 residues

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 8 summaries

Database : fetch1rng.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		25	15.2	25	1	AAT89069	Identification of
2		21	12.7	21	1	ADR46309	Early growth respo
3		19	11.5	21	1	ADM86425	Oligo #1 used for
	c 4	19	11.5	21	1	ADM86426	Oligo #2 used for
5		19	11.5	21	1	ADN31474	Small interfering
	c 6	19	11.5	21	1	ADN31475	Small interfering
7		19	11.5	21	1	AEA63988	Egr-1 gene siRNA o
	c 8	19	11.5	21	1	AEA63989	Egr-1 gene siRNA o

ALIGNMENTS

RESULT 1
AAT89069
ID AAT89069 standard; DNA; 25 BP.
XX
AC AAT89069;
XX
DT 20-APR-1998 (first entry)
XX
DE Identification of prostate disease marker using Egr1 specific primer 1.
XX
KW Prostate cancer; biomarker; human; probe; Egr1; amplification; treatment;
KW RT-PCR; primer; early growth response gene 1; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9736535-A2.
XX
PD 09-OCT-1997.
XX
PF 28-MAR-1997; 97WO-US005335.
XX
PR 29-MAR-1996; 96US-00626169.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Russell DW, Thigpen AE;
XX
DR WPI; 1997-502799/46.
XX
PT Disease marker probes for human prostate cancer - specific for Egr1 and
PT DTDST nucleotide sequences.
XX
PS Example 1; Page 73; 93pp; English.
XX
CC This is an Early groth response gene 1 (Egr1) specific primer. This is
CC used for the RT-PCR amplification of the Egr1 mRNAs. The mRNA encoding
CC Egr1 is significantly increased in prostate tumours. This is used in a
CC method for identifying disease marker probes for human prostate cancer.
CC The method comprises providing human prostate RNAs and amplifying the
CC RNAs to provide nucleic acid amplification products. These amplification
CC products are separated and the RNAs that are differentially expressed
CC between human prostate cancers versus normal or benign human prostate are
CC identified. The biomarker probes can be used to detect prostate cancer in
CC a biological sample. In particular the probes hybridise to Egr1 (Genbank
CC Ref. P18146) or DTDST (Genbank Ref. U14528 and D42049) nucleotide
CC sequences. Antibodies immunoreactive with peptides encoded by the nucleic
CC acids can be used for treatment of prostate cancer
XX
SQ Sequence 25 BP; 5 A; 8 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 15.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 ATGGCCGCGGCCAAGGCCGAGATGC 295
||||||||||||||||||||||||
Db 1 ATGGCCGCGGCCAAGGCCGAGATGC 25

RESULT 2
ADR46309
ID ADR46309 standard; DNA; 21 BP.
XX
AC ADR46309;
XX
DT 18-NOV-2004 (first entry)
XX
DE Early growth response 1 forward PCR primer.
XX
KW Early growth response 1; Bex4; ovarian cancer; cytostatic; human;
KW gene therapy; tumour suppressor protein; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2004072269-A2.
XX
PD 26-AUG-2004.
XX
PF 12-FEB-2004; 2004WO-US004413.
XX
PR 12-FEB-2003; 2003US-0446877P.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
PI Shridhar V, Chien J;
XX
DR WPI; 2004-625868/60.
XX
PT New vector comprising an isolated nucleic acid encoding a Bex4
PT polypeptide, useful for treating cancer, e.g. ovarian, cervical, brain,
PT breast, prostate or liver cancer.
XX

PS Example 1; SEQ ID NO 22; 47pp; English.
XX
CC The present sequence is that of a forward PCR primer for early growth
CC response 1. The primer was used in a semiquantitative RT-PCR in an
CC examination of the differential expression of genes in ovarian tumour
CC cell lines, and in early-stage and late-stage primary tumours. The
CC invention is based on the discovery that Bex4 (or proapoptotic protein on
CC chromosome X (PAPX)) ADR46296 is down-regulated in cancer cells. Claimed
CC methods for killing a tumour cell comprise administering to the tumour a
CC nucleic acid that encodes a Bex4 polypeptide, a vector comprising the
CC nucleic acid, or a Bex4 polypeptide. The tumour cell is selected from an
CC ovarian, cervical, brain, breast, prostate and hepatic tumour cell.
CC Detection of a lower than normal level of Bex4 polypeptide in cells in a
CC sample indicates a predisposition of an individual to develop cancer. A
CC claimed method for detecting cancer recurrence in an individual diagnosed
CC with and treated for cancer comprises measuring the level of bex4 gene
CC methylation. The presence of hypermethylation indicates recurrence. The
CC cancer is ovarian, breast, prostate, cervical, brain or liver cancer.
XX
SQ Sequence 21 BP; 4 A; 10 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 12.7%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 GACACCAGCTCTCCAGCCTGC 261
||||||||||||||||||||
Db 1 GACACCAGCTCTCCAGCCTGC 21

RESULT 3
ADM86425
ID ADM86425 standard; RNA; 21 BP.
XX
AC ADM86425;
XX
DT 03-JUN-2004 (first entry)
XX
DE Oligo #1 used for synthesis of human Egr-1 gene siRNA.
XX
KW Interfering RNA; RNAi; cell proliferation; cell migration;
KW epithelial cell; smooth muscle cell; lymphocyte; myocardial infarction;
KW hyperproliferative cell growth; cancer; chronic lymphatic leukaemia;
KW immune-mediated inflammatory diseases; rheumatoid arthritis;
KW multiple sclerosis; diabetes; psoriasis; restenosis; cosmetic;
KW small-interfering RNA; siRNA; human; Egr-1;
KW early growth response factor-1; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 20. .21
FT /*tag= a
FT /label= Deoxyribonucleotides overhang
FT /note= "The 3' end of the complementary strand overhangs
FT the 5' end of this sequence by the sequence TT"
XX
PN US2003157030-A1.
XX
PD 21-AUG-2003.
XX
PF 04-NOV-2002; 2002US-00288230.
XX
PR 02-NOV-2001; 2001US-0336314P.
PR 05-NOV-2001; 2001US-0337304P.
PR 15-OCT-2002; 2002US-0418909P.
XX
PA (INSE-) INSERT THERAPEUTICS INC.
XX
PI Davis ME, Jensen GS, Pun SH;
XX
DR WPI; 2004-119048/12.
XX
PT Formulations containing interfering RNA, useful for e.g. treating cancer,
PT for delivery by inhalation, percutaneously or by electroporation, or as
PT coating on medical device.
XX
PS Disclosure; Page 21; 53pp; English.
XX
CC The invention relates to stable respiratory formulation comprising an
CC interfering RNA (RNAi) construct for pulmonary or nasal delivery to the
CC lungs. The RNAi constructs are used to inhibit target genes, particularly
CC for reducing cell proliferation and/or migration, especially of
CC epithelial or smooth muscle cells, also to reduce activation of
CC lymphocytes. Preferred applications are treatment (or prevention) of
CC myocardial infarction; hyperproliferative cell growth (cancers,
CC particularly chronic lymphatic leukaemia); immune-mediated inflammatory
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes and
CC psoriasis) or restenosis. The RNAi construct can also be used in
CC cosmetics. The present sequence is an oligonucleotide used in the
CC synthesis of small-interfering RNA (siRNA) which is targetted to human
CC early growth response factor -1 (Egr-1) gene.
XX
SQ Sequence 21 BP; 2 A; 6 C; 8 G; 2 T; 3 U; 0 Other;

Query Match 11.5%; Score 19; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 2.8;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 262 TCGTCCAGGATGGCCGCGG 280
:||:||||||:||||||||
Db 1 UCGUCCAGGAUGGCCGCGG 19

RESULT 4
ADM86426/c
ID ADM86426 standard; RNA; 21 BP.
XX
AC ADM86426;
XX
DT 03-JUN-2004 (first entry)
XX
DE Oligo #2 used for synthesis of human Egr-1 gene siRNA.
XX
KW Interfering RNA; RNAi; cell proliferation; cell migration;
KW epithelial cell; smooth muscle cell; lymphocyte; myocardial infarction;
KW hyperproliferative cell growth; cancer; chronic lymphatic leukaemia;
KW immune-mediated inflammatory diseases; rheumatoid arthritis;
KW multiple sclerosis; diabetes; psoriasis; restenosis; cosmetic;
KW small-interfering RNA; siRNA; human; Egr-1;
KW early growth response factor-1; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 20. .21
FT /*tag= a
FT /label= Deoxyribonucleotides overhang
FT /note= "The 3' end of the complementary strand overhangs
FT the 5' end of this sequence by the sequence TT"
XX
PN US2003157030-A1.
XX
PD 21-AUG-2003.
XX
PF 04-NOV-2002; 2002US-00288230.
XX
PR 02-NOV-2001; 2001US-0336314P.
PR 05-NOV-2001; 2001US-0337304P.
PR 15-OCT-2002; 2002US-0418909P.
XX
PA (INSE-) INSERT THERAPEUTICS INC.
XX
PI Davis ME, Jensen GS, Pun SH;
XX
DR WPI; 2004-119048/12.

XX
PT Formulations containing interfering RNA, useful for e.g. treating cancer,
PT for delivery by inhalation, percutaneously or by electroporation, or as
PT coating on medical device.
XX
PS Disclosure; Page 21; 53pp; English.
XX
CC The invention relates to stable respiratory formulation comprising an
CC interfering RNA (RNAi) construct for pulmonary or nasal delivery to the
CC lungs. The RNAi constructs are used to inhibit target genes, particularly
CC for reducing cell proliferation and/or migration, especially of
CC epithelial or smooth muscle cells, also to reduce activation of
CC lymphocytes. Preferred applications are treatment (or prevention) of
CC myocardial infarction; hyperproliferative cell growth (cancers,
CC particularly chronic lymphatic leukaemia); immune-mediated inflammatory
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes and
CC psoriasis) or restenosis. The RNAi construct can also be used in
CC cosmetics. The present sequence is an oligonucleotide used in the
CC synthesis of small-interfering RNA (siRNA) which is targetted to human
CC early growth response factor -1 (Egr-1) gene.
XX
SQ Sequence 21 BP; 3 A; 8 C; 6 G; 2 T; 2 U; 0 Other;

Query Match 11.5%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 TCGTCCAGGATGGCCGCGG 280
||||||||||||||||||||
Db 19 TCGTCCAGGATGGCCGCGG 1

RESULT 5
ADN31474
ID ADN31474 standard; DNA; 21 BP.
XX
AC ADN31474;
XX
DT 17-JUN-2004 (first entry)
XX
DE Small interfering RNA (siRNA) oligonucleotide #3.
XX
KW RNA interference; small-interfering RNA; siRNA; angiogenesis;
KW ischaemic damage; apoptosis; hyperplastic cell growth; cancer;
KW inflammatory disorders; smooth muscle cell; restenosis; epithelial cell;
KW cosmetic; myocardial infarction; neointimal hyperplasia; atherosclerosis;
KW neoplastic cell growth; anaplastic cell growth; tumour;
KW chronic lymphatic leukaemia; rheumatoid arthritis; multiple sclerosis;
KW diabetes; psoriasis; acute renal failure; reperfusion injury;
KW renal isograft survival; vasoconstrictor; blood pressure; hypertension;
KW DNA-RNA hybrid; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 1. .19
FT /*tag= a
FT /label= RNA
XX
PN US2004063654-A1.
XX
PD 01-APR-2004.
XX
PF 15-MAY-2003; 2003US-00440506.
XX
PR 02-NOV-2001; 2001US-0336314P.
PR 05-NOV-2001; 2001US-0337304P.
PR 15-OCT-2002; 2002US-0418909P.
PR 04-NOV-2002; 2002US-00288230.
XX
PA (DAVI/) DAVIS M E.
PA (JENS/) JENSEN G S.
PA (PUNS/) PUN S H.
XX
PI Davis ME, Jensen GS, Pun SH;
XX
DR WPI; 2004-346270/32.
XX
PT Attenuating expression of target gene of cell in vivo useful for treating
PT e.g. myocardial infarction and cancer, involves administering RNAi
PT constructs e.g. small interfering RNA formulated in supramolecular
PT complex or liposome.
XX
PS Example 1; Page 23; 39pp; English.
XX
CC The invention relates to a method of attenuating expression of a target
CC gene of a cell in vivo which, involves administering RNAi constructs (I),
CC formulated in a supramolecular complex or liposomes in an amount
CC sufficient to attenuate expression of the target gene through an RNA
CC interference mechanisms, and thus alter the growth, survival or
CC differentiation of treated cells. (I) is an small-interfering RNA (siRNA)
CC which is 19-30 base pairs long; an expression vector having a coding
CC sequence that is transcribed to produce one or more transcriptional
CC products that produce siRNA in the treated cells; or a hairpin RNA which
CC is processed to siRNA in the treated cells. (I) is useful for attenuating
CC expression of a gene resulting in increased angiogenesis and/or reduced
CC ischaemic damage in and around a myocardial infarct. (I) is systemically
CC available and attenuates expression of one or more genes in cells distal
CC to the pericardial space. (I) inhibits proliferation of the cell or
CC promotes apoptosis of the cell. (I) is used for the treatment of
CC hyperplastic cell growth, such as cancer, inhibiting activation of
CC lymphocytes for treatment or prophylaxis of immune mediated inflammatory
CC disorders, inhibiting proliferation of smooth muscle cells, for treatment
CC or prophylaxis of restenosis, or inhibiting proliferation of epithelial
CC cells, for cosmetic preparation. (I) is used for reducing proliferation
CC and/or migration of smooth muscle cells and for treating myocardial
CC infarction. The method is useful for treating myocardial infarction,
CC preventing apoptosis of cell, and cancer, for treatment or prophylaxis of
CC immune mediated inflammatory disorders and restenosis, for inhibiting
CC proliferation of epithelial cells and thus (I) is useful as a component
CC of cosmetic preparations. The method is also useful for treating
CC neointimal hyperplasia such as restenosis and atherosclerosis, for
CC treatment or prophylaxis of neoplastic, anaplastic and/or hyperplastic
CC cell growth, tumour, for anti-cancer treatment, and chronic lymphatic
CC leukaemia, rheumatoid arthritis, inflammation and inflammation related
CC diseases such as multiple sclerosis and diabetes, psoriasis, acute renal
CC failure, reperfusion injury and prolonging renal isograft survival, and
CC for reducing expression of vasoconstrictors or reducing receptor levels
CC of vasoconstrictor, reducing blood pressure in patients suffering from
CC systemic and pulmonary hypertension. The present sequence represents an
CC oligonucleotide used to synthesise siRNA used in the method of the
CC invention.
XX
SQ Sequence 21 BP; 2 A; 6 C; 8 G; 2 T; 3 U; 0 Other;

Query Match 11.5%; Score 19; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 2.8;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 262 TCGTCCAGGATGGCCGCGG 280
:||:||||||:||||||||
Db 1 UCGUCCAGGAUGGCCGCGG 19

RESULT 6
ADN31475/c
ID ADN31475 standard; DNA; 21 BP.
XX
AC ADN31475;
XX
DT 17-JUN-2004 (first entry)
XX
DE Small interfering RNA (siRNA) oligonucleotide #4.
XX
KW RNA interference; small-interfering RNA; siRNA; angiogenesis;
KW ischaemic damage; apoptosis; hyperplastic cell growth; cancer;

KW inflammatory disorders; smooth muscle cell; restenosis; epithelial cell;
KW cosmetic; myocardial infarction; neointimal hyperplasia; atherosclerosis;
KW neoplastic cell growth; anaplastic cell growth; tumour;
KW chronic lymphatic leukaemia; rheumatoid arthritis; multiple sclerosis;
KW diabetes; psoriasis; acute renal failure; reperfusion injury;
KW renal isograft survival; vasoconstrictor; blood pressure; hypertension;
KW DNA-RNA hybrid; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 1. .19
FT /*tag= a
FT /label= RNA
XX
PN US2004063654-A1.
XX
PD 01-APR-2004.
XX
PF 15-MAY-2003; 2003US-00440506.
XX
PR 02-NOV-2001; 2001US-0336314P.
PR 05-NOV-2001; 2001US-0337304P.
PR 15-OCT-2002; 2002US-0418909P.
PR 04-NOV-2002; 2002US-00288230.
XX
PA (DAVI/) DAVIS M E.
PA (JENS/) JENSEN G S.
PA (PUNS/) PUN S H.
XX
PI Davis ME, Jensen GS, Pun SH;
XX
DR WPI; 2004-346270/32.
XX
PT Attenuating expression of target gene of cell in vivo useful for treating
PT e.g. myocardial infarction and cancer, involves administering RNAi
PT constructs e.g. small interfering RNA formulated in supramolecular
PT complex or liposome.
XX
PS Example 1; Page 23; 39pp; English.
XX
CC The invention relates to a method of attenuating expression of a target
CC gene of a cell in vivo which, involves administering RNAi constructs (I),
CC formulated in a supramolecular complex or liposomes in an amount
CC sufficient to attenuate expression of the target gene through an RNA
CC interference mechanisms, and thus alter the growth, survival or
CC differentiation of treated cells. (I) is an small-interfering RNA (siRNA)
CC which is 19-30 base pairs long; an expression vector having a coding
CC sequence that is transcribed to produce one or more transcriptional
CC products that produce siRNA in the treated cells; or a hairpin RNA which
CC is processed to siRNA in the treated cells. (I) is useful for attenuating
CC expression of a gene resulting in increased angiogenesis and/or reduced
CC ischaemic damage in and around a myocardial infarct. (I) is systemically
CC available and attenuates expression of one or more genes in cells distal
CC to the pericardial space. (I) inhibits proliferation of the cell or
CC promotes apoptosis of the cell. (I) is used for the treatment of
CC hyperplastic cell growth, such as cancer, inhibiting activation of
CC lymphocytes for treatment or prophylaxis of immune mediated inflammatory
CC disorders, inhibiting proliferation of smooth muscle cells for treatment
CC or prophylaxis of restenosis, or inhibiting proliferation of epithelial
CC cells, for cosmetic preparation. (I) is used for reducing proliferation
CC and/or migration of smooth muscle cells and for treating myocardial
CC infarction. The method is useful for treating myocardial infarction,
CC preventing apoptosis of cell, and cancer, for treatment or prophylaxis of
CC immune mediated inflammatory disorders and restenosis, for inhibiting
CC proliferation of epithelial cells and thus (I) is useful as a component
CC of cosmetic preparations. The method is also useful for treating
CC neointimal hyperplasia such as restenosis and atherosclerosis, for
CC treatment or prophylaxis of neoplastic, anaplastic and/or hyperplastic
CC cell growth, tumour, for anti-cancer treatment, and chronic lymphatic
CC leukaemia, rheumatoid arthritis, inflammation and inflammation related
CC diseases such as multiple sclerosis and diabetes, psoriasis, acute renal
CC failure, reperfusion injury and prolonging renal isograft survival, and
CC for reducing expression of vasoconstrictors or reducing receptor levels
CC of vasoconstrictor, reducing blood pressure in patients suffering from
CC systemic and pulmonary hypertension. The present sequence represents an
CC oligonucleotide used to synthesise siRNA used in the method of the
CC invention.
XX
SQ Sequence 21 BP; 3 A; 8 C; 6 G; 2 T; 2 U; 0 Other;

Query Match 11.5%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 TCGTCCAGGATGGCCGCGG 280
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Db 19 TCGTCCAGGATGGCCGCGG 1

RESULT 7
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ID AEA63988 standard; RNA; 21 BP.
XX
AC AEA63988;
XX
DT 25-AUG-2005 (first entry)
XX
DE Egr-1 gene siRNA oligonucleotide SEQ ID NO:7.
XX
KW RNA interference; cytostatic; short interfering RNA; siRNA;
KW gene silencing; early growth response factor-1; ds; DNA-RNA hybrid.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 20. .21
FT /*tag= a
FT /note= "2 thymine overhang"
XX
PN US2005136430-A1.
XX
PD 23-JUN-2005.
XX
PF 15-JUL-2004; 2004US-00892527.
XX
PR 15-JUL-2003; 2003US-0487570P.
PR 08-DEC-2003; 2003US-0528143P.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Davis ME;
XX
DR WPI; 2005-457504/46.
XX
PT New double-stranded nucleic acid comprising a DNA sense polynucleotide
PT strand having modifications, and an RNA antisense polynucleotide strand,
PT useful for inhibiting expression of a target gene by an RNA interference
PT mechanism.
XX
PS Disclosure; SEQ ID NO 7; 31pp; English.
XX
CC The invention relates to a double-stranded nucleic acid comprising a DNA
CC sense polynucleotide strand with one or more modifications or modified
CC nucleotides, and an RNA antisense polynucleotide strand having a
CC designated sequence that hybridizes to at least a portion of a transcript
CC of the target gene and is sufficient to inhibit expression of the target
CC gene. Also described: (1) a pharmaceutical preparation for delivery of an
CC RNA interference (RNAi) nucleic acid to an organism, the composition
CC comprising a carrier and the double-stranded nucleic acid; (2) a
CC pharmaceutical package comprising the pharmaceutical preparation, in
CC association with instructions for administering the preparation to a
CC human patient; (3) a method for decreasing the expression of a target
CC gene in a cell, or one or more cells of the subject by contacting the
CC cell with a composition comprising the double-stranded nucleic acid; (4)
CC a coating for use on a surface of a medical device, comprising a polymer

CC matrix having RNAi constructs dispersed in it, which RNAi constructs are
CC eluted from the matrix when implanted at site in a patient's body and
CC alter the growth, survival or differentiation of cells in the vicinity of
CC the implanted device, where at least one of the RNAi constructs is the
CC double-stranded nucleic acid; (5) a method of optimizing an RNAi
CC construct for pharmaceutical uses; and (6) a method of optimizing an RNAi
CC construct comprising generating a plurality of test RNAi constructs, each
CC of the construct comprising the double-stranded nucleic acid; and
CC determining gene silencing effect of the test RNAi constructs. The double
CC stranded nucleic acid is useful for inhibiting expression of a target
CC gene by an RNA interference mechanism. The present sequence represents an
CC exemplary early growth response factor 1 (Egr-1) gene siRNA
CC oligonucleotide, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 21 BP; 2 A; 6 C; 8 G; 2 T; 3 U; 0 Other;

Query Match 11.5%; Score 19; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 2.8;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy        262 TCGTCCAGGATGGCCGCGG 280
              :||:|||||||:||||||||
Db          1 UCGUCCAGGAUGGCCGCGG 19
```

RESULT 8
AEA63989/c
ID AEA63989 standard; RNA; 21 BP.
XX
AC AEA63989;
XX
DT 25-AUG-2005 (first entry)
XX
DE Egr-1 gene siRNA oligonucleotide SEQ ID NO:8.
XX
KW RNA interference; cytostatic; short interfering RNA; siRNA;
KW gene silencing; early growth response factor-1; ds; DNA-RNA hybrid.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 20. .21
FT /*tag= a
FT /note= "2 thymine overhang"
XX
PN US2005136430-A1.
XX
PD 23-JUN-2005.
XX
PF 15-JUL-2004; 2004US-00892527.
XX
PR 15-JUL-2003; 2003US-0487570P.
PR 08-DEC-2003; 2003US-0528143P.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Davis ME;
XX
DR WPI; 2005-457504/46.
XX
PT New double-stranded nucleic acid comprising a DNA sense polynucleotide
PT strand having modifications, and an RNA antisense polynucleotide strand,
PT useful for inhibiting expression of a target gene by an RNA interference
PT mechanism.
XX
PS Disclosure; SEQ ID NO 8; 31pp; English.
XX
CC The invention relates to a double-stranded nucleic acid comprising a DNA
CC sense polynucleotide strand with one or more modifications or modified
CC nucleotides, and an RNA antisense polynucleotide strand having a
CC designated sequence that hybridizes to at least a portion of a transcript
CC of the target gene and is sufficient to inhibit expression of the target
CC gene. Also described: (1) a pharmaceutical preparation for delivery of an
CC RNA interference (RNAi) nucleic acid to an organism, the composition
CC comprising a carrier and the double-stranded nucleic acid; (2) a
CC pharmaceutical package comprising the pharmaceutical preparation, in
CC association with instructions for administering the preparation to a
CC human patient; (3) a method for decreasing the expression of a target
CC gene in a cell, or one or more cells of the subject by contacting the
CC cell with a composition comprising the double-stranded nucleic acid; (4)
CC a coating for use on a surface of a medical device, comprising a polymer
CC matrix having RNAi constructs dispersed in it, which RNAi constructs are
CC eluted from the matrix when implanted at site in a patient's body and
CC alter the growth, survival or differentiation of cells in the vicinity of
CC the implanted device, where at least one of the RNAi constructs is the
CC double-stranded nucleic acid; (5) a method of optimizing an RNAi
CC construct for pharmaceutical uses; and (6) a method of optimizing an RNAi
CC construct comprising generating a plurality of test RNAi constructs, each
CC of the construct comprising the double-stranded nucleic acid; and
CC determining gene silencing effect of the test RNAi constructs. The double
CC stranded nucleic acid is useful for inhibiting expression of a target
CC gene by an RNA interference mechanism. The present sequence represents an
CC exemplary early growth response factor 1 (Egr-1) gene siRNA
CC oligonucleotide, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 21 BP; 3 A; 8 C; 6 G; 2 T; 2 U; 0 Other;

Query Match 11.5%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        262 TCGTCCAGGATGGCCGCGG 280
              ||||||||||||||||||||
Db         19 TCGTCCAGGATGGCCGCGG 1
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Search completed: February 7, 2006, 13:38:54
Job time : 0.001 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 13:43:27 ; Search time 1 Seconds
(without alignments)
0.135 Million cell updates/sec

Title: US-09-889-075-1
Perfect score: 165
Sequence: 1 cgcatgtaacccggccaggc.....cagatctctgacccgttcgg 165

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 19 seqs, 408 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 19 summaries

Database : fetch1rnpbn.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	25	15.2	25	1	US-10-310-914A-146665	Sequence 146665,
c	2	24	14.5	24	1	US-10-310-914A-146627	Sequence 146627,
c	3	23	13.9	23	1	US-10-310-914A-146657	Sequence 146657,
c	4	23	13.9	23	1	US-10-310-914A-146662	Sequence 146662,
c	5	22	13.3	22	1	US-10-310-914A-146614	Sequence 146614,
c	6	22	13.3	22	1	US-10-310-914A-146654	Sequence 146654,
c	7	20	12.1	20	1	US-10-310-914A-146637	Sequence 146637,
	8	20	12.1	20	1	US-11-082-731A-4	Sequence 4, Appli
c	9	20	12.1	20	1	US-11-082-731A-5	Sequence 5, Appli
	10	20	12.1	20	1	US-11-082-731A-6	Sequence 6, Appli
c	11	20	12.1	20	1	US-11-082-731A-7	Sequence 7, Appli
	12	19	11.5	21	1	US-11-044-677-7	Sequence 7, Appli
c	13	19	11.5	21	1	US-11-044-677-8	Sequence 8, Appli
c	14	18.4	11.2	23	1	US-10-310-914A-118426	Sequence 118426,
	15	17.8	10.8	21	1	US-10-310-914A-1278264	Sequence 1278264,
c	16	17.8	10.8	21	1	US-10-310-914A-496892	Sequence 496892,
	17	16.8	10.2	21	1	US-10-310-914A-1163792	Sequence 1163792,
c	18	16.8	10.2	21	1	US-10-310-914A-696870	Sequence 696870,
c	19	16	9.7	20	1	US-10-310-914A-168458	Sequence 168458,

ALIGNMENTS

RESULT 1
US-10-310-914A-146665/c
; Sequence 146665, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 146665
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-146665

Query Match 15.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 GCCCCGGGCTGCACCCCCCCGCCCC 240
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Db 25 GCCCCGGGCTGCACCCCCCCGCCCC 1

RESULT 2
US-10-310-914A-146627/c
; Sequence 146627, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 146627
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-146627

Query Match 14.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 24 GTCCCCTGCAGCTCCAGCCCCGGG 1

RESULT 3
US-10-310-914A-146657/c
; Sequence 146657, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01 .
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 146657
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-146657

Query Match 13.9%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        216 GCCCCGGGCTGCACCCCCCCGCC 238
              ||||||||||||||||||||||||
Db         23 GCCCCGGGCTGCACCCCCCCGCC 1


RESULT 4
US-10-310-914A-146662/c
; Sequence 146662, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 146662
;   LENGTH: 23
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-146662

  Query Match             13.9%;  Score 23;  DB 1;  Length 23;
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  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        217 CCCCGGGCTGCACCCCCCCGCCC 239
              |||||||||||||||||||||||
Db         23 CCCCGGGCTGCACCCCCCCGCCC 1


RESULT 5
US-10-310-914A-146614/c
; Sequence 146614, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A.
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 146614
;   LENGTH: 22
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-146614

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  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        205 CTGCAGCTCCAGCCCCGGGCTG 226
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RESULT 6
US-10-310-914A-146654/c
; Sequence 146654, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
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; SEQ ID NO 146654
;   LENGTH: 22
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-146654

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  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        196 CGGTGTCCCCTGCAGCTCCAGC 217
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Db         22 CGGTGTCCCCTGCAGCTCCAGC 1


RESULT 7
US-10-310-914A-146637/c
; Sequence 146637, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 146637
;   LENGTH: 20
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-146637

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  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 8
US-11-082-731A-4
; Sequence 4, Application US/11082731A
; Publication No. US20050261226A1
; GENERAL INFORMATION:
;  APPLICANT: Mercola, Daniel
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
;  TITLE OF INVENTION:  OF CANCER WITH OLIGONUCLEOTIDES DIRECTED
;  TITLE OF INVENTION:  AGAINST EGR-1
;  FILE REFERENCE: MER.003.P
;  CURRENT APPLICATION NUMBER: US/11/082,731A
;  CURRENT FILING DATE:  2005-03-17
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-11-082-731A-4

  Query Match             12.1%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db          1 GCGGCCAAGGCCGAGATGCA 20


RESULT 9
US-11-082-731A-5/c
; Sequence 5, Application US/11082731A
; Publication No. US20050261226A1
; GENERAL INFORMATION:
;  APPLICANT: Mercola, Daniel
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
;  TITLE OF INVENTION:  OF CANCER WITH OLIGONUCLEOTIDES DIRECTED
;  TITLE OF INVENTION:  AGAINST EGR-1
;  FILE REFERENCE: MER.003.P
;  CURRENT APPLICATION NUMBER: US/11/082,731A
;  CURRENT FILING DATE:  2005-03-17
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-11-082-731A-5

  Query Match             12.1%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        277 GCGGCCAAGGCCGAGATGCA 296
              ||||||||||||||||||||
Db         20 GCGGCCAAGGCCGAGATGCA 1


RESULT 10
US-11-082-731A-6
; Sequence 6, Application US/11082731A
; Publication No. US20050261226A1
; GENERAL INFORMATION:
;  APPLICANT: Mercola, Daniel
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
;  TITLE OF INVENTION:  OF CANCER WITH OLIGONUCLEOTIDES DIRECTED
;  TITLE OF INVENTION:  AGAINST EGR-1
;  FILE REFERENCE: MER.003.P
;  CURRENT APPLICATION NUMBER: US/11/082,731A
;  CURRENT FILING DATE:  2005-03-17
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-11-082-731A-6

  Query Match             12.1%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        308 CGCTGCAGATCTCTGACCCG 327
              ||||||||||||||||||||
Db          1 CGCTGCAGATCTCTGACCCG 20


RESULT 11
US-11-082-731A-7/c
; Sequence 7, Application US/11082731A
; Publication No. US20050261226A1
; GENERAL INFORMATION:
;  APPLICANT: Mercola, Daniel
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
;  TITLE OF INVENTION:  OF CANCER WITH OLIGONUCLEOTIDES DIRECTED
;  TITLE OF INVENTION:  AGAINST EGR-1
;  FILE REFERENCE: MER.003.P
;  CURRENT APPLICATION NUMBER: US/11/082,731A
;  CURRENT FILING DATE:  2005-03-17
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-11-082-731A-7

  Query Match             12.1%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        308 CGCTGCAGATCTCTGACCCG 327
              ||||||||||||||||||||
Db         20 CGCTGCAGATCTCTGACCCG 1


RESULT 12
US-11-044-677-7
; Sequence 7, Application US/11044677
; Publication No. US20050256071A1
; GENERAL INFORMATION:
;  APPLICANT: Davis, Mark E.
;  TITLE OF INVENTION: INHIBITOR NUCLEIC ACIDS
;  FILE REFERENCE: CTCH-P02-020
;  CURRENT APPLICATION NUMBER: US/11/044,677
;  CURRENT FILING DATE:  2005-01-27
;  PRIOR APPLICATION NUMBER: US 10/892,527
;  PRIOR FILING DATE: 2004-07-15
;  PRIOR APPLICATION NUMBER: US 60/487,570
;  PRIOR FILING DATE: 2003-07-15
;  PRIOR APPLICATION NUMBER: US 60/528,143
;  PRIOR FILING DATE: 2003-12-08
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically synthesized
US-11-044-677-7

  Query Match             11.5%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 6.6;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        262 TCGTCCAGGATGGCCGCGG 280
              :||:|||||:||||||||
Db          1 UCGUCCAGGAUGGCCGCGG 19


RESULT 13
US-11-044-677-8/c
; Sequence 8, Application US/11044677
; Publication No. US20050256071A1
; GENERAL INFORMATION:
;  APPLICANT: Davis, Mark E.
;  TITLE OF INVENTION: INHIBITOR NUCLEIC ACIDS
;  FILE REFERENCE: CTCH-P02-020
;  CURRENT APPLICATION NUMBER: US/11/044,677
;  CURRENT FILING DATE:  2005-01-27
;  PRIOR APPLICATION NUMBER: US 10/892,527
;  PRIOR FILING DATE: 2004-07-15
```

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;  PRIOR APPLICATION NUMBER: US 60/487,570
;  PRIOR FILING DATE: 2003-07-15
;  PRIOR APPLICATION NUMBER: US 60/528,143
;  PRIOR FILING DATE: 2003-12-08
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically synthesized
US-11-044-677-8

  Query Match             11.5%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        262 TCGTCCAGGATGGCCGCGG 280
              ||||||||||||||||||||
Db         19 TCGTCCAGGATGGCCGCGG 1


RESULT 14
US-10-310-914A-118426/c
; Sequence 118426, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 118426
;   LENGTH: 23
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-118426

  Query Match             11.2%;  Score 18.4;  DB 1;  Length 23;
  Best Local Similarity   95.0%;  Pred. No. 6.7;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        241 GACACCAGCTCTCCAGCCTG 260
              || ||||||||||||||||||
Db         23 GAGACCAGCTCTCCAGCCTG 4


RESULT 15
US-10-310-914A-1278264
; Sequence 1278264, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1278264
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-1278264

  Query Match             10.8%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 8.3;
  Matches   17;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        208 CAGCTCCAGCCCCGGGCTGCA 228
              ||||:|||||||||| :| |
Db          1 CAGCUCCAGCCCCGGGAUGAA 21


RESULT 16
US-10-310-914A-496892/c
; Sequence 496892, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 496892
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-496892

  Query Match             10.8%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 8.3;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        205 CTGCAGCTCCAGCCCCGGGCT 225
              |||| ||||| ||||||||||
Db         21 CTGCCGCTCCCGCCCCGGGCT 1


RESULT 17
US-10-310-914A-1163792
; Sequence 1163792, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1163792
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-1163792

  Query Match             10.2%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   70.0%;  Pred. No. 10;
  Matches   14;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        293 TGCAGCTGATGTCCCCGCTG 312
              :|||||:|| |:| ||||:|
Db          2 UGCAGCUGAGGUCACCGCUG 21


RESULT 18
US-10-310-914A-696870/c
; Sequence 696870, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
```

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 696870
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-696870

Query Match 10.2%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        219 CCGGGCTGCACCCCCCCGCC 238
              ||||||||| ||| ||||||
Db         21 CCGGGCTGCCCCCTCCCGCC 2
```

RESULT 19
US-10-310-914A-168458/c
; Sequence 168458, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 168458
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-168458

Query Match 9.7%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        243 CACCAGCTCTCCAGCC 258
              ||||||||||||||||
Db         17 CACCAGCTCTCCAGCC 2
```

Search completed: February 7, 2006, 13:43:28
Job time : 1 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 18:38:34 ; Search time 97 Seconds
(without alignments)
604.737 Million cell updates/sec

Title: US-09-889-075-6
Perfect score: 33
Sequence: 1 ccgcggccaggctagctacaacgacctggacga 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1074460

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	63.6	32	3	US-09-270-140A-19	Sequence 19, Appl
	2	20.8	63.0	31	3	US-09-605-558B-76	Sequence 76, Appl
	3	20.8	63.0	31	3	US-10-144-094-76	Sequence 76, Appl
	4	19.8	60.0	32	3	US-09-270-140A-28	Sequence 28, Appl
	5	18.4	55.8	29	3	US-09-270-140A-25	Sequence 25, Appl
	6	18.4	55.8	31	3	US-09-270-140A-51	Sequence 51, Appl
	7	18	54.5	30	3	US-09-270-140A-55	Sequence 55, Appl
	8	18	54.5	31	3	US-09-270-140A-42	Sequence 42, Appl
	9	17.4	52.7	31	3	US-09-253-955-5	Sequence 5, Appli
	10	17.4	52.7	31	3	US-09-637-405-5	Sequence 5, Appli
	11	17.4	52.7	31	3	US-09-746-985B-5	Sequence 5, Appli
	12	16.8	50.9	29	3	US-09-270-140A-23	Sequence 23, Appl
	13	16.8	50.9	31	3	US-09-270-140A-48	Sequence 48, Appl
	14	16.4	49.7	31	3	US-09-270-140A-45	Sequence 45, Appl
	15	16	48.5	16	3	US-09-536-393-19	Sequence 19, Appl
	16	16	48.5	32	3	US-09-270-140A-12	Sequence 12, Appl
	17	16	48.5	32	3	US-09-270-140A-58	Sequence 58, Appl
	18	15.6	47.3	16	3	US-09-866-316B-15	Sequence 15, Appl
	19	15.4	46.7	30	3	US-09-231-899-74	Sequence 74, Appl
c	20	15.4	46.7	33	3	US-09-446-634-16	Sequence 16, Appl
	21	15.2	46.1	32	3	US-09-270-140A-15	Sequence 15, Appl
	22	15	45.5	16	3	US-09-536-393-20	Sequence 20, Appl
	23	14.8	44.8	24	2	US-08-880-829-17	Sequence 17, Appl
c	24	14.8	44.8	25	3	US-09-396-196G-33280	Sequence 33280, A
c	25	14.8	44.8	25	3	US-09-396-196G-33281	Sequence 33281, A
c	26	14.8	44.8	25	3	US-09-396-196G-33282	Sequence 33282, A
c	27	14.6	44.2	30	2	US-08-384-708A-9	Sequence 9, Appli
c	28	14.6	44.2	30	3	US-08-687-421-9	Sequence 9, Appli
c	29	14.6	44.2	30	3	US-08-442-423-9	Sequence 9, Appli
c	30	14.4	43.6	25	3	US-09-396-196G-71213	Sequence 71213, A
	31	14.4	43.6	26	3	US-09-419-788-36	Sequence 36, Appl
	32	14.4	43.6	31	3	US-08-454-899G-48	Sequence 48, Appl
c	33	14.4	43.6	31	3	US-08-454-899G-49	Sequence 49, Appl
	34	14.2	43.0	32	2	US-08-530-492-75	Sequence 75, Appl
	35	14.2	43.0	32	3	US-08-906-517-75	Sequence 75, Appl
	36	14	42.4	25	3	US-09-396-196G-32934	Sequence 32934, A
c	37	14	42.4	27	3	US-09-254-180C-46	Sequence 46, Appl
	38	14	42.4	27	3	US-09-254-180C-91	Sequence 91, Appl
	39	14	42.4	33	2	US-08-438-639-55	Sequence 55, Appl
	40	14	42.4	33	2	US-07-813-338A-55	Sequence 55, Appl
	41	13.8	41.8	21	3	US-09-657-472-1431	Sequence 1431, Ap
	42	13.8	41.8	25	3	US-09-396-196G-37381	Sequence 37381, A
	43	13.8	41.8	25	3	US-09-396-196G-43577	Sequence 43577, A
c	44	13.8	41.8	25	3	US-09-396-196G-121924	Sequence 121924,
c	45	13.8	41.8	25	3	US-09-396-196G-125801	Sequence 125801,

ALIGNMENTS

RESULT 1
US-09-270-140A-19
; Sequence 19, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J&J1799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
; OTHER INFORMATION: H-ras codon 61, position 3
US-09-270-140A-19

Query Match 63.6%; Score 21; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 CGGCCAGGCTAGCTACAACGA 24
              |||||||||||||||||||||
Db          6 CGGCCAGGCTAGCTACAACGA 26
```

RESULT 2
US-09-605-558B-76
; Sequence 76, Application US/09605558B
; Patent No. 6706474
; GENERAL INFORMATION:
; APPLICANT: LU, YI
; APPLICANT: LI, JING
; TITLE OF INVENTION: NUCLEIC ACID ENZYME BIOSENSORS FOR IONS
; FILE REFERENCE: 10322/6
; CURRENT APPLICATION NUMBER: US/09/605,558B
; CURRENT FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1

```
; SEQ ID NO 76
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic chimeric
;   OTHER INFORMATION: substrate
;   OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic chimeric
;   OTHER INFORMATION: substrate
US-09-605-558B-76

  Query Match             63.0%;  Score 20.8;  DB 3;  Length 31;
  Best Local Similarity   91.7%;  Pred. No. 36;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGCGGCCAGGCTAGCTACAACGAC 25
              |||  ||||||||||||||||||||
Db          1 CGCACCCAGGCTAGCTACAACGAC 24


RESULT 3
US-10-144-094-76
; Sequence 76, Application US/10144094
; Patent No. 6890719
; GENERAL INFORMATION:
;  APPLICANT: LU, YI
;  APPLICANT:  LIU, JUEWEN
;  TITLE OF INVENTION: NEW FLUORESCENCE BASED BIOSENSOR
;  FILE REFERENCE: 10322/44
;  CURRENT APPLICATION NUMBER: US/10/144,094
;  CURRENT FILING DATE:  2002-05-10
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic chimeric
;   OTHER INFORMATION: substrate
;   FEATURE:
;   OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic chimeric
;   OTHER INFORMATION: substrate
US-10-144-094-76

  Query Match             63.0%;  Score 20.8;  DB 3;  Length 31;
  Best Local Similarity   91.7%;  Pred. No. 36;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CGCGGCCAGGCTAGCTACAACGAC 25
              |||  ||||||||||||||||||||
Db          1 CGCACCCAGGCTAGCTACAACGAC 24


RESULT 4
US-09-270-140A-28
; Sequence 28, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
;  APPLICANT: Todd, Alison
;  APPLICANT:  Fuery, Caroline
;  APPLICANT:  Cairns, Murray
;  TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
;  FILE REFERENCE: J&J1799
;  CURRENT APPLICATION NUMBER: US/09/270,140A
;  CURRENT FILING DATE:  1999-03-16
;  PRIOR APPLICATION NUMBER: 60/079,651
;  PRIOR FILING DATE: 1998-03-27
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 32
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:DNAzyme
US-09-270-140A-28

  Query Match             60.0%;  Score 19.8;  DB 3;  Length 32;
  Best Local Similarity   84.0%;  Pred. No. 91;
  Matches   21;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CCAGGCTAGCTACAACGACCTGGAC 31
              | :|||||||||||||| ||| ||
Db          7 CARGGCTAGCTACAACGATCTGTAC 31


RESULT 5
US-09-270-140A-25
; Sequence 25, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
;  APPLICANT: Todd, Alison
;  APPLICANT:  Fuery, Caroline
;  APPLICANT:  Cairns, Murray
;  TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
;  FILE REFERENCE: J&J1799
;  CURRENT APPLICATION NUMBER: US/09/270,140A
;  CURRENT FILING DATE:  1999-03-16
;  PRIOR APPLICATION NUMBER: 60/079,651
;  PRIOR FILING DATE: 1998-03-27
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
;   OTHER INFORMATION: N-ras codon 61, position 1
US-09-270-140A-25

  Query Match             55.8%;  Score 18.4;  DB 3;  Length 29;
  Best Local Similarity   95.0%;  Pred. No. 3.2e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGGCTAGCTACAACGACCTG 28
              ||||||||||||||||||| |
Db          9 AGGCTAGCTACAACGACCAG 28


RESULT 6
US-09-270-140A-51
; Sequence 51, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
;  APPLICANT: Todd, Alison
;  APPLICANT:  Fuery, Caroline
;  APPLICANT:  Cairns, Murray
;  TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
;  FILE REFERENCE: J&J1799
;  CURRENT APPLICATION NUMBER: US/09/270,140A
;  CURRENT FILING DATE:  1999-03-16
;  PRIOR APPLICATION NUMBER: 60/079,651
;  PRIOR FILING DATE: 1998-03-27
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
;   OTHER INFORMATION: Codon 51 - mutant (G to A)
US-09-270-140A-51
```

Query Match 55.8%; Score 18.4; DB 3; Length 31;
Best Local Similarity 78.6%; Pred. No. 3.3e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          3 GCGGCCAGGCTAGCTACAACGACCTGGA 30
              | ||  |||||||||||||||||   ||
Db          3 GTGGAGAGGCTAGCTACAACGACAACGA 30
```

RESULT 7
US-09-270-140A-55
; Sequence 55, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J&J1799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
; OTHER INFORMATION: codon 508 - mutant (CTT deletion) for Cystic
; OTHER INFORMATION: fibrosis
US-09-270-140A-55

Query Match 54.5%; Score 18; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 CCAGGCTAGCTACAACGA 24
              ||||||||||||||||||
Db          6 CCAGGCTAGCTACAACGA 23
```

RESULT 8
US-09-270-140A-42
; Sequence 42, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J&J1799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
; OTHER INFORMATION: codon 542 - Cystic Fibrosis
US-09-270-140A-42

Query Match 54.5%; Score 18; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 CCAGGCTAGCTACAACGA 24
              ||||||||||||||||||
Db          8 CCAGGCTAGCTACAACGA 25
```

RESULT 9
US-09-253-955-5
; Sequence 5, Application US/09253955
; Patent No. 6140055
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; TITLE OF INVENTION: Molecules And Kits
; FILE REFERENCE: JJ1770SequenceListing
; CURRENT APPLICATION NUMBER: US/09/253,955
; CURRENT FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: 60/076,899
; EARLIER FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 31
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-253-955-5

Query Match 52.7%; Score 17.4; DB 3; Length 31;
Best Local Similarity 77.8%; Pred. No. 8.1e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          4 CGGCCAGGCTAGCTACAACGACCTGGA 30
              | |  |||||||||||||||||  || |
Db          3 CTGAAAGGCTAGCTACAACGAATTGCA 29
```

RESULT 10
US-09-637-405-5
; Sequence 5, Application US/09637405
; Patent No. 6201113
; GENERAL INFORMATION:
; APPLICANT: Todd, Alison V
; APPLICANT: Fuery, Caroline J
; APPLICANT: Cairns, Murray J
; TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related
; TITLE OF INVENTION: Molecules And Kits
; FILE REFERENCE: JJ1770SequenceListing
; CURRENT APPLICATION NUMBER: US/09/637,405
; CURRENT FILING DATE: 2000-08-11
; EARLIER APPLICATION NUMBER: 09/253,955
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 31
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-637-405-5

Query Match 52.7%; Score 17.4; DB 3; Length 31;
Best Local Similarity 77.8%; Pred. No. 8.1e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          4 CGGCCAGGCTAGCTACAACGACCTGGA 30
              | |  |||||||||||||||||  || |
Db          3 CTGAAAGGCTAGCTACAACGAATTGCA 29
```

RESULT 11
US-09-746-985B-5
; Sequence 5, Application US/09746985B
; Patent No. 6365724

```
; GENERAL INFORMATION:
;  APPLICANT: Todd, Alison V
;  APPLICANT:  Fuery, Caroline J
;  APPLICANT:  Cairns, Murray J
;  TITLE OF INVENTION: Zymogenic Nucleic Acid Detection Methods, And Related.
;  TITLE OF INVENTION:  Molecules And Kits
;  FILE REFERENCE: SequenceListing
;  CURRENT APPLICATION NUMBER: US/09/746,985B
;  CURRENT FILING DATE:  2000-12-21
;  PRIOR APPLICATION NUMBER: 60/076,899
;  PRIOR FILING DATE: 1998-03-05
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR primer
US-09-746-985B-5

  Query Match             52.7%;  Score 17.4;  DB 3;  Length 31;
  Best Local Similarity   77.8%;  Pred. No. 8.1e+02;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          4 CGGCCAGGCTAGCTACAACGACCTGGA 30
              | |  |||||||||||||||  || |
Db          3 CTGAAAGGCTAGCTACAACGAATTGCA 29


RESULT 12
US-09-270-140A-23
; Sequence 23, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
;  APPLICANT: Todd, Alison
;  APPLICANT:  Fuery, Caroline
;  APPLICANT:  Cairns, Murray
;  TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
;  FILE REFERENCE: J&J1799
;  CURRENT APPLICATION NUMBER: US/09/270,140A
;  CURRENT FILING DATE:  1999-03-16
;  PRIOR APPLICATION NUMBER: 60/079,651
;  PRIOR FILING DATE: 1998-03-27
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
;   OTHER INFORMATION: N-ras codon 61 position 1 - mutant (C to A, G or
;   OTHER INFORMATION: U)
US-09-270-140A-23

  Query Match             50.9%;  Score 16.8;  DB 3;  Length 29;
  Best Local Similarity   90.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GGCCAGGCTAGCTACAACGA 24
              ||  ||||||||||||||||
Db          4 GGADAGGCTAGCTACAACGA 23


RESULT 13
US-09-270-140A-48
; Sequence 48, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
;  APPLICANT: Todd, Alison
;  APPLICANT:  Fuery, Caroline
;  APPLICANT:  Cairns, Murray
;  TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
;  FILE REFERENCE: J&J1799
;  CURRENT APPLICATION NUMBER: US/09/270,140A
;  CURRENT FILING DATE:  1999-03-16
;  PRIOR APPLICATION NUMBER: 60/079,651
;  PRIOR FILING DATE: 1998-03-27
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
;   OTHER INFORMATION: Codon 551 -  wildtype
US-09-270-140A-48

  Query Match             50.9%;  Score 16.8;  DB 3;  Length 31;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+03;
  Matches   21;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 GCGGCCAGGCTAGCTACAACGACCTGGA 30
              | ||   ||||||||||||||||   ||
Db          3 GTGGAGGGGCTAGCTACAACGACAACGA 30


RESULT 14
US-09-270-140A-45
; Sequence 45, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
;  APPLICANT: Todd, Alison
;  APPLICANT:  Fuery, Caroline
;  APPLICANT:  Cairns, Murray
;  TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
;  FILE REFERENCE: J&J1799
;  CURRENT APPLICATION NUMBER: US/09/270,140A
;  CURRENT FILING DATE:  1999-03-16
;  PRIOR APPLICATION NUMBER: 60/079,651
;  PRIOR FILING DATE: 1998-03-27
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:DNAzyme for
;   OTHER INFORMATION: cystic Fibrosis Codon 542 - mutant (G to U)
US-09-270-140A-45

  Query Match             49.7%;  Score 16.4;  DB 3;  Length 31;
  Best Local Similarity   94.4%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CCAGGCTAGCTACAACGA 24
              | ||||||||||||||||
Db          8 CAAGGCTAGCTACAACGA 25


RESULT 15
US-09-536-393-19
; Sequence 19, Application US/09536393
; Patent No. 6562570
; GENERAL INFORMATION:
;  APPLICANT: Rossi, John J.
;  APPLICANT: Scherr, Michaela
;  APPLICANT: Riggs, Arthur D.
;  TITLE OF INVENTION: Method for Identifying Accessible Binding Sites on RNA
;  FILE REFERENCE: 1954-285
;  CURRENT APPLICATION NUMBER: US/09/536,393
;  CURRENT FILING DATE: 2000-03-28
;  EARLIER APPLICATION NUMBER: 60/127,529
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; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAzyme core
US-09-536-393-19

Query Match 48.5%; Score 16; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          9 AGGCTAGCTACAACGA 24
              ||||||||||||||||
Db          1 AGGCTAGCTACAACGA 16
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Search completed: February 4, 2006, 19:49:04
Job time : 98 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 18:39:41 ; Search time 533 Seconds
(without alignments)
511.988 Million cell updates/sec

Title: US-09-889-075-6
Perfect score: 33
Sequence: 1 ccgcggccaggctagctacaacgacctggacga 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

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Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	33	100.0	33	6	US-10-133-226-8	Sequence 8, Appli
2	28.8	87.3	33	6	US-10-133-226-9	Sequence 9, Appli
3	25.4	77.0	31	6	US-10-238-700-4166	Sequence 4166, Ap
4	25.4	77.0	31	9	US-10-724-270-4166	Sequence 4166, Ap
5	25.2	76.4	31	3	US-09-930-423-3786	Sequence 3786, Ap
6	25.2	76.4	31	3	US-09-745-237A-3786	Sequence 3786, Ap
7	24.6	74.5	31	3	US-09-780-533A-5246	Sequence 5246, Ap
8	24.6	74.5	31	3	US-09-848-754A-6564	Sequence 6564, Ap
9	24.6	74.5	31	6	US-10-238-700-1337	Sequence 1337, Ap
10	24.6	74.5	31	9	US-10-724-270-2344	Sequence 2344, Ap
11	24.2	73.3	31	3	US-09-827-395A-1983	Sequence 1983, Ap
12	24.2	73.3	31	6	US-10-430-882-1983	Sequence 1983, Ap
13	24	72.7	31	3	US-09-740-332-6223	Sequence 6223, Ap
14	24	72.7	31	3	US-09-740-332-6424	Sequence 6424, Ap
15	24	72.7	31	3	US-09-817-879-6223	Sequence 6223, Ap
16	24	72.7	31	3	US-09-817-879-6424	Sequence 6424, Ap
17	24	72.7	31	7	US-10-669-841-12768	Sequence 12768, A
18	24	72.7	31	7	US-10-669-841-12969	Sequence 12969, A
19	23.8	72.1	31	7	US-10-138-674-17622	Sequence 17622, A
20	23.8	72.1	31	7	US-10-287-949A-17622	Sequence 17622, A
21	23.8	72.1	31	8	US-10-712-633-2842	Sequence 2842, Ap
22	23.8	72.1	33	9	US-10-479-832A-63	Sequence 63, Appl
23	23.6	71.5	31	3	US-09-792-818-1717	Sequence 1717, Ap
24	23.6	71.5	31	5	US-10-163-552-994	Sequence 994, App
25	23.6	71.5	31	6	US-10-238-700-4531	Sequence 4531, Ap
26	23.6	71.5	31	6	US-10-230-006-1827	Sequence 1827, Ap
27	23.6	71.5	31	9	US-10-724-270-4531	Sequence 4531, Ap
28	23.6	71.5	31	9	US-10-724-270-5649	Sequence 5649, Ap
29	23.6	71.5	33	9	US-10-479-832A-39	Sequence 39, Appl
30	23.4	70.9	31	3	US-09-930-423-3733	Sequence 3733, Ap
31	23.4	70.9	31	3	US-09-740-332-6029	Sequence 6029, Ap
32	23.4	70.9	31	3	US-09-740-332-8754	Sequence 8754, Ap
33	23.4	70.9	31	3	US-09-745-237A-3733	Sequence 3733, Ap
34	23.4	70.9	31	3	US-09-817-879-6029	Sequence 6029, Ap
35	23.4	70.9	31	3	US-09-817-879-8754	Sequence 8754, Ap
36	23.4	70.9	31	5	US-10-163-552-1319	Sequence 1319, Ap
37	23.4	70.9	31	7	US-10-669-841-12574	Sequence 12574, A
38	23.4	70.9	31	7	US-10-669-841-15299	Sequence 15299, A
39	23.4	70.9	31	9	US-10-724-270-5974	Sequence 5974, Ap
40	23.2	70.3	31	3	US-09-848-754A-6965	Sequence 6965, Ap
41	23.2	70.3	31	3	US-09-740-332-4836	Sequence 4836, Ap
42	23.2	70.3	31	3	US-09-817-879-4836	Sequence 4836, Ap
43	23.2	70.3	31	7	US-10-138-674-17079	Sequence 17079, A
44	23.2	70.3	31	7	US-10-287-949A-17079	Sequence 17079, A
45	23.2	70.3	31	7	US-10-669-841-11381	Sequence 11381, A

ALIGNMENTS

RESULT 1
US-10-133-226-8
; Sequence 8, Application US/10133226
; Publication No. US20030203864A1
; GENERAL INFORMATION:
; APPLICANT: Khachigian, Michael L.
; TITLE OF INVENTION: TREATMENT OF CANCER
; FILE REFERENCE: 529282000500
; CURRENT APPLICATION NUMBER: US/10/133,226
; CURRENT FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: PCT/AU00/01315
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAenzyme
US-10-133-226-8

Query Match 100.0%; Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCGGCCAGGCTAGCTACAACGACCTGGACGA 33
||||||||||||||||||||||||||||||||||
Db 1 CCGCGGCCAGGCTAGCTACAACGACCTGGACGA 33

RESULT 2
US-10-133-226-9
; Sequence 9, Application US/10133226
; Publication No. US20030203864A1
; GENERAL INFORMATION:
; APPLICANT: Khachigian, Michael L.
; TITLE OF INVENTION: TREATMENT OF CANCER
; FILE REFERENCE: 529282000500
; CURRENT APPLICATION NUMBER: US/10/133,226
; CURRENT FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: PCT/AU00/01315
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9

; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNAenzyme
US-10-133-226-9

Query Match 87.3%; Score 28.8; DB 6; Length 33;
Best Local Similarity 93.8%; Pred. No. 0.008;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 CCGCGGCCAGGCTAGCTACAACGACCTGGACG 32
              |||| ||||||||||||||||||||| |||||
Db          1 CCGCTGCCAGGCTAGCTACAACGACCCGGACG 32
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RESULT 3
US-10-238-700-4166
; Sequence 4166, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4166
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-238-700-4166

Query Match 77.0%; Score 25.4; DB 6; Length 31;
Best Local Similarity 96.3%; Pred. No. 0.26;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 GCGGCCAGGCTAGCTACAACGACCTGG 29
              |||||| ||||||||||||||||||||
Db          2 GCGGCCGGGCTAGCTACAACGACCTGG 28
```

RESULT 4
US-10-724-270-4166
; Sequence 4166, Application US/10724270
; Publication No. US20050080031A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; TITLE OF INVENTION: RAS, HER2 and HIV
; FILE REFERENCE: 400/046-US (MBHB02-326-A)
; CURRENT APPLICATION NUMBER: US/10/724,270
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/US02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/238,700
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/157,580
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4166
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-724-270-4166

Query Match 77.0%; Score 25.4; DB 9; Length 31;
Best Local Similarity 96.3%; Pred. No. 0.26;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 GCGGCCAGGCTAGCTACAACGACCTGG 29
              |||||| ||||||||||||||||||||
Db          2 GCGGCCGGGCTAGCTACAACGACCTGG 28
```

RESULT 5
US-09-930-423-3786
; Sequence 3786, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3786
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-3786

Query Match 76.4%; Score 25.2; DB 3; Length 31;
Best Local Similarity 90.0%; Pred. No. 0.32;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGAC 31
              ||| ||| ||||||||||||||||||| ||
Db          1 CGCTGCCGGGCTAGCTACAACGACCTGAAC 30
```

RESULT 6
US-09-745-237A-3786
; Sequence 3786, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3786
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-745-237A-3786

Query Match 76.4%; Score 25.2; DB 3; Length 31;
Best Local Similarity 90.0%; Pred. No. 0.32;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGAC 31
              ||| ||| |||||||||||||||||||| ||
Db          1 CGCTGCCGGGCTAGCTACAACGACCTGAAC 30
```

RESULT 7
US-09-780-533A-5246
; Sequence 5246, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5246
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-5246

Query Match 74.5%; Score 24.6; DB 3; Length 31;
Best Local Similarity 87.1%; Pred. No. 0.59;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGACG 32
              ||||| ||||||||||||||||  | ||||
Db          1 CGCGGGCAGGCTAGCTACAACGAGGTCGACG 31
```

RESULT 8
US-09-848-754A-6564
; Sequence 6564, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6564
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-6564

Query Match 74.5%; Score 24.6; DB 3; Length 31;
Best Local Similarity 87.1%; Pred. No. 0.59;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGACG 32
              | ||||| |||||||||||||||||| ||| |
Db          1 CCCGGCCGGGCTAGCTACAACGACCCGGAGG 31
```

RESULT 9
US-10-238-700-1337
; Sequence 1337, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1337
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-238-700-1337

Query Match 74.5%; Score 24.6; DB 6; Length 31;
Best Local Similarity 87.1%; Pred. No. 0.59;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGACG 32
              ||| |||||||||||||||||||| | | ||
Db          1 CGCCGCCAGGCTAGCTACAACGACTTCGCCG 31
```

RESULT 10
US-10-724-270-2344
; Sequence 2344, Application US/10724270
; Publication No. US20050080031A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; TITLE OF INVENTION: RAS, HER2 and HIV
; FILE REFERENCE: 400/046-US (MBHB02-326-A)
; CURRENT APPLICATION NUMBER: US/10/724,270
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/US02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/238,700
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/157,580
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853

; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2344
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-724-270-2344

Query Match 74.5%; Score 24.6; DB 9; Length 31;
Best Local Similarity 87.1%; Pred. No. 0.59;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGACG 32
              ||| |||||||||||||||||||| | | ||
Db          1 CGCCGCCAGGCTAGCTACAACGACTTCGCCG 31
```

RESULT 11
US-09-827-395A-1983
; Sequence 1983, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1983
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Definition of Artificial Sequence: Enzymatic Nucleic Acid
US-09-827-395A-1983

Query Match 73.3%; Score 24.2; DB 3; Length 31;
Best Local Similarity 89.7%; Pred. No. 0.89;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGA 30
              | ||| |||||||||||||||| |||||
Db          1 CTCGGGCAGGCTAGCTACAACGAGCTGGA 29
```

RESULT 12
US-10-430-882-1983
; Sequence 1983, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haeberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1983
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Definition of Artificial Sequence: Enzymatic Nucleic Acid
US-10-430-882-1983

Query Match 73.3%; Score 24.2; DB 6; Length 31;
Best Local Similarity 89.7%; Pred. No. 0.89;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGA 30
              | ||| |||||||||||||||| |||||
Db          1 CTCGGGCAGGCTAGCTACAACGAGCTGGA 29
```

RESULT 13
US-09-740-332-6223
; Sequence 6223, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6223
; LENGTH: 31
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: DNAzyme
US-09-740-332-6223

Query Match 72.7%; Score 24; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 GCGGCCAGGCTAGCTACAACGACC 26
              ||||||||||||||||||||||||
Db          2 GCGGCCAGGCTAGCTACAACGACC 25
```

RESULT 14
US-09-740-332-6424
; Sequence 6424, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6424
; LENGTH: 31
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: DNAzyme
US-09-740-332-6424

Query Match 72.7%; Score 24; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCGGCCAGGCTAGCTACAACGACC 26
||||||||||||||||||||||||
Db 2 GCGGCCAGGCTAGCTACAACGACC 25

RESULT 15
US-09-817-879-6223
; Sequence 6223, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6223
; LENGTH: 31
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: DNAzyme
US-09-817-879-6223

Query Match 72.7%; Score 24; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCGGCCAGGCTAGCTACAACGACC 26
||||||||||||||||||||||||
Db 2 GCGGCCAGGCTAGCTACAACGACC 25

Search completed: February 4, 2006, 19:58:11
Job time : 534 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 18:41:57 ; Search time 307 Seconds
(without alignments)
90.086 Million cell updates/sec

Title: US-09-889-075-6
Perfect score: 33
Sequence: 1 ccgcggccaggctagctacaacgacctggacga 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
11: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20.8	63.0	31	8	US-11-082-197-76	Sequence 76, Appl
	2	19.6	59.4	33	8	US-11-056-620-10	Sequence 10, Appl
	3	19.4	58.8	33	8	US-11-056-620-16	Sequence 16, Appl
	4	19	57.6	33	8	US-11-056-620-6	Sequence 6, Appli
	5	19	57.6	33	8	US-11-056-620-22	Sequence 22, Appl
	6	18.4	55.8	33	8	US-11-056-620-14	Sequence 14, Appl
	7	18	54.5	33	8	US-11-056-620-3	Sequence 3, Appli
	8	17.8	53.9	33	8	US-11-056-620-11	Sequence 11, Appl
	9	17.6	53.3	33	8	US-11-056-620-8	Sequence 8, Appli
	10	17.2	52.1	23	7	US-10-310-914A-934309	Sequence 934309,
	11	17	51.5	33	8	US-11-056-620-12	Sequence 12, Appl
	12	16.4	49.7	33	8	US-11-056-620-7	Sequence 7, Appli
	13	16.4	49.7	33	8	US-11-056-620-17	Sequence 17, Appl
	14	16.4	49.7	33	8	US-11-056-620-18	Sequence 18, Appl
	15	16.4	49.7	33	8	US-11-056-620-23	Sequence 23, Appl
	16	16.4	49.7	33	8	US-11-056-620-29	Sequence 29, Appl
	17	16	48.5	33	8	US-11-056-620-4	Sequence 4, Appli
	18	16	48.5	33	8	US-11-056-620-5	Sequence 5, Appli
	19	16	48.5	33	8	US-11-056-620-13	Sequence 13, Appl
	20	15.8	47.9	33	8	US-11-056-620-2	Sequence 2, Appli
	21	15.6	47.3	33	8	US-11-056-620-15	Sequence 15, Appl
c	22	15.4	46.7	25	8	US-11-121-849-230037	Sequence 230037,
	23	15.4	46.7	25	8	US-11-136-527-123370	Sequence 123370,
	24	15.4	46.7	25	8	US-11-136-527-349343	Sequence 349343,
	25	15.4	46.7	33	8	US-11-056-620-9	Sequence 9, Appli
	26	15.4	46.7	33	8	US-11-056-620-19	Sequence 19, Appl
	27	15.2	46.1	24	7	US-10-310-914A-1044460	Sequence 1044460,
	28	15.2	46.1	25	8	US-11-121-849-134816	Sequence 134816,
	29	15	45.5	15	8	US-11-070-871-3	Sequence 3, Appli
	30	15	45.5	15	8	US-11-070-871-14	Sequence 14, Appl
	31	15	45.5	19	9	US-11-101-244-1084037	Sequence 1084037,
	32	15	45.5	19	9	US-11-101-244-1084136	Sequence 1084136,
	33	15	45.5	19	10	US-11-083-784-1084037	Sequence 1084037,
	34	15	45.5	19	10	US-11-083-784-1084136	Sequence 1084136,
	35	15	45.5	24	7	US-10-310-914A-972510	Sequence 972510,
c	36	15	45.5	25	8	US-11-136-527-216259	Sequence 216259,
c	37	15	45.5	25	8	US-11-136-527-216280	Sequence 216280,
c	38	15	45.5	25	8	US-11-136-527-338829	Sequence 338829,
	39	15	45.5	33	8	US-11-056-620-1	Sequence 1, Appli
	40	15	45.5	33	8	US-11-056-620-20	Sequence 20, Appl
	41	15	45.5	33	8	US-11-056-620-28	Sequence 28, Appl
	42	14.8	44.8	19	9	US-11-101-244-1051196	Sequence 1051196,
	43	14.8	44.8	19	10	US-11-083-784-1051196	Sequence 1051196,
c	44	14.8	44.8	22	7	US-10-310-914A-145807	Sequence 145807,
c	45	14.8	44.8	23	7	US-10-310-914A-145829	Sequence 145829,

ALIGNMENTS

RESULT 1
US-11-082-197-76
; Sequence 76, Application US/11082197
; Publication No. US20050282186A1
; GENERAL INFORMATION:
; APPLICANT: LU, YI
; APPLICANT: LIU, JUEWEN
; TITLE OF INVENTION: NEW FLUORESCENCE BASED BIOSENSOR
; FILE REFERENCE: 10322/44
; CURRENT APPLICATION NUMBER: US/11/082,197
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US/10/144,094
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic chimeric
; OTHER INFORMATION: substrate
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic chimeric
; OTHER INFORMATION: substrate
US-11-082-197-76

Query Match 63.0%; Score 20.8; DB 8; Length 31;
Best Local Similarity 91.7%; Pred. No. 9.9;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 CGCGGCCAGGCTAGCTACAACGAC 25
              |||  ||||||||||||||||||||
Db          1 CGCACCCAGGCTAGCTACAACGAC 24
```

RESULT 2
US-11-056-620-10
; Sequence 10, Application US/11056620
; Publication No. US20060019914A1
; GENERAL INFORMATION:
; APPLICANT: Pourmotabbed, Tayebeh
; APPLICANT: Hasegawa, Hisashi
; APPLICANT: Batson, Chad
; TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND INVASION BY ANTI-MATRIX

; TITLE OF INVENTION: METALLOPROTEINASE DNAZYMES
; FILE REFERENCE: 1306-22-2
; CURRENT APPLICATION NUMBER: US/11/056,620
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,490
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Anti-human MMP-9 DNAzyme
US-11-056-620-10

Query Match 59.4%; Score 19.6; DB 8; Length 33;
Best Local Similarity 84.6%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          7 CCAGGCTAGCTACAACGACCTGGACG 32
              | ||||||||||||||| ||  |||
Db          7 CGAGGCTAGCTACAACGATCTCCACG 32
```

RESULT 3
US-11-056-620-16
; Sequence 16, Application US/11056620
; Publication No. US20060019914A1
; GENERAL INFORMATION:
; APPLICANT: Pourmotabbed, Tayebeh
; APPLICANT: Hasegawa, Hisashi
; APPLICANT: Batson, Chad
; TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND INVASION BY ANTI-MATRIX
; TITLE OF INVENTION: METALLOPROTEINASE DNAZYMES
; FILE REFERENCE: 1306-22-2
; CURRENT APPLICATION NUMBER: US/11/056,620
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,490
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Negative control DNAzyme
US-11-056-620-16

Query Match 58.8%; Score 19.4; DB 8; Length 33;
Best Local Similarity 95.2%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          6 GCCAGGCTAGCTACAACGACC 26
              |||||||||||||||||| |
Db          6 GCCAGGCTAGCTACAACGATC 26
```

RESULT 4
US-11-056-620-6
; Sequence 6, Application US/11056620
; Publication No. US20060019914A1
; GENERAL INFORMATION:
; APPLICANT: Pourmotabbed, Tayebeh
; APPLICANT: Hasegawa, Hisashi
; APPLICANT: Batson, Chad
; TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND INVASION BY ANTI-MATRIX
; TITLE OF INVENTION: METALLOPROTEINASE DNAZYMES
; FILE REFERENCE: 1306-22-2
; CURRENT APPLICATION NUMBER: US/11/056,620
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,490
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Anti-human MMP-9 DNAzyme
US-11-056-620-6

Query Match 57.6%; Score 19; DB 8; Length 33;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 GCCAGGCTAGCTACAACGA 24
              |||||||||||||||||||
Db          6 GCCAGGCTAGCTACAACGA 24
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RESULT 5
US-11-056-620-22
; Sequence 22, Application US/11056620
; Publication No. US20060019914A1
; GENERAL INFORMATION:
; APPLICANT: Pourmotabbed, Tayebeh
; APPLICANT: Hasegawa, Hisashi
; APPLICANT: Batson, Chad
; TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND INVASION BY ANTI-MATRIX
; TITLE OF INVENTION: METALLOPROTEINASE DNAZYMES
; FILE REFERENCE: 1306-22-2
; CURRENT APPLICATION NUMBER: US/11/056,620
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,490
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Anti-rat MMP-9 DNAzyme
US-11-056-620-22

Query Match 57.6%; Score 19; DB 8; Length 33;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          6 GCCAGGCTAGCTACAACGA 24
              |||||||||||||||||||
Db          6 GCCAGGCTAGCTACAACGA 24
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RESULT 6
US-11-056-620-14
; Sequence 14, Application US/11056620
; Publication No. US20060019914A1
; GENERAL INFORMATION:
; APPLICANT: Pourmotabbed, Tayebeh
; APPLICANT: Hasegawa, Hisashi
; APPLICANT: Batson, Chad
; TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND INVASION BY ANTI-MATRIX
; TITLE OF INVENTION: METALLOPROTEINASE DNAZYMES
; FILE REFERENCE: 1306-22-2
; CURRENT APPLICATION NUMBER: US/11/056,620
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,490
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 33

```
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Negative control DNAzyme
US-11-056-620-14

  Query Match             55.8%;  Score 18.4;  DB 8;  Length 33;
  Best Local Similarity   95.0%;  Pred. No. 97;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GCCAGGCTAGCTACAACGAC 25
              | ||||||||||||||||||
Db          6 GACAGGCTAGCTACAACGAC 25


RESULT 7
US-11-056-620-3
; Sequence 3, Application US/11056620
; Publication No. US20060019914A1
; GENERAL INFORMATION:
;  APPLICANT: Pourmotabbed, Tayebeh
;  APPLICANT:  Hasegawa, Hisashi
;  APPLICANT:  Batson, Chad
;  TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND INVASION BY ANTI-MATRIX
;  TITLE OF INVENTION:  METALLOPROTEINASE DNAZYMES
;  FILE REFERENCE: 1306-22-2
;  CURRENT APPLICATION NUMBER: US/11/056,620
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: US 60/543,490
;  PRIOR FILING DATE: 2004-02-11
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
;   LENGTH: 33
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Anti-human MMP-9 DNAzyme
US-11-056-620-3

  Query Match             54.5%;  Score 18;  DB 8;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CAGGCTAGCTACAACGAC 25
              ||||||||||||||||||
Db          8 CAGGCTAGCTACAACGAC 25


RESULT 8
US-11-056-620-11
; Sequence 11, Application US/11056620
; Publication No. US20060019914A1
; GENERAL INFORMATION:
;  APPLICANT: Pourmotabbed, Tayebeh
;  APPLICANT:  Hasegawa, Hisashi
;  APPLICANT:  Batson, Chad
;  TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND INVASION BY ANTI-MATRIX
;  TITLE OF INVENTION:  METALLOPROTEINASE DNAZYMES
;  FILE REFERENCE: 1306-22-2
;  CURRENT APPLICATION NUMBER: US/11/056,620
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: US 60/543,490
;  PRIOR FILING DATE: 2004-02-11
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
;   LENGTH: 33
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Anti-human MMP-9 DNAzyme
US-11-056-620-11

  Query Match             53.9%;  Score 17.8;  DB 8;  Length 33;
  Best Local Similarity   90.5%;  Pred. No. 1.7e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 CAGGCTAGCTACAACGACCTG 28
              ||||||||||||||||||  ||
Db          8 CAGGCTAGCTACAACGAGGTG 28


RESULT 9
US-11-056-620-8
; Sequence 8, Application US/11056620
; Publication No. US20060019914A1
; GENERAL INFORMATION:
;  APPLICANT: Pourmotabbed, Tayebeh
;  APPLICANT:  Hasegawa, Hisashi
;  APPLICANT:  Batson, Chad
;  TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND INVASION BY ANTI-MATRIX
;  TITLE OF INVENTION:  METALLOPROTEINASE DNAZYMES
;  FILE REFERENCE: 1306-22-2
;  CURRENT APPLICATION NUMBER: US/11/056,620
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: US 60/543,490
;  PRIOR FILING DATE: 2004-02-11
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
;   LENGTH: 33
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Anti-human MMP-9 DNAzyme
US-11-056-620-8

  Query Match             53.3%;  Score 17.6;  DB 8;  Length 33;
  Best Local Similarity   83.3%;  Pred. No. 2.1e+02;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCGCGGCCAGGCTAGCTACAACGA 24
              || | |  ||||||||||||||||
Db          1 CCCCAGAGAGGCTAGCTACAACGA 24


RESULT 10
US-10-310-914A-934309
; Sequence 934309, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 934309
;   LENGTH: 23
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-934309

  Query Match             52.1%;  Score 17.2;  DB 7;  Length 23;
  Best Local Similarity   77.3%;  Pred. No. 2.9e+02;
  Matches   17;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCGCGGCCAGGCTAGCTACAAC 22
              |||||||| || :|||:| |||
Db          2 CCGCGGCCGGGGUAGCUAUAAC 23
```

```
RESULT 11
US-11-056-620-12
; Sequence 12, Application US/11056620
; Publication No. US20060019914A1
; GENERAL INFORMATION:
;  APPLICANT: Pourmotabbed, Tayebeh
;  APPLICANT:  Hasegawa, Hisashi
;  APPLICANT:  Batson, Chad
;  TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND INVASION BY ANTI-MATRIX
;  TITLE OF INVENTION:  METALLOPROTEINASE DNAZYMES
;  FILE REFERENCE: 1306-22-2
;  CURRENT APPLICATION NUMBER: US/11/056,620
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: US 60/543,490
;  PRIOR FILING DATE: 2004-02-11
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 33
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Anti-human MMP-2 DNAzyme
US-11-056-620-12

  Query Match             51.5%;  Score 17;  DB 8;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CAGGCTAGCTACAACGA 24
              |||||||||||||||||
Db          8 CAGGCTAGCTACAACGA 24


RESULT 12
US-11-056-620-7
; Sequence 7, Application US/11056620
; Publication No. US20060019914A1
; GENERAL INFORMATION:
;  APPLICANT: Pourmotabbed, Tayebeh
;  APPLICANT:  Hasegawa, Hisashi
;  APPLICANT:  Batson, Chad
;  TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND INVASION BY ANTI-MATRIX
;  TITLE OF INVENTION:  METALLOPROTEINASE DNAZYMES
;  FILE REFERENCE: 1306-22-2
;  CURRENT APPLICATION NUMBER: US/11/056,620
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: US 60/543,490
;  PRIOR FILING DATE: 2004-02-11
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
;   LENGTH: 33
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Anti-human MMP-9 DNAzyme
US-11-056-620-7

  Query Match             49.7%;  Score 16.4;  DB 8;  Length 33;
  Best Local Similarity   94.4%;  Pred. No. 6.4e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGGCTAGCTACAACGACC 26
              |||||||||||||||| |
Db          9 AGGCTAGCTACAACGATC 26


RESULT 13
US-11-056-620-17
; Sequence 17, Application US/11056620
; Publication No. US20060019914A1
; GENERAL INFORMATION:
;  APPLICANT: Pourmotabbed, Tayebeh
;  APPLICANT:  Hasegawa, Hisashi
;  APPLICANT:  Batson, Chad
;  TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND INVASION BY ANTI-MATRIX
;  TITLE OF INVENTION:  METALLOPROTEINASE DNAZYMES
;  FILE REFERENCE: 1306-22-2
;  CURRENT APPLICATION NUMBER: US/11/056,620
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: US 60/543,490
;  PRIOR FILING DATE: 2004-02-11
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
;   LENGTH: 33
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Negative control DNAzyme
US-11-056-620-17

  Query Match             49.7%;  Score 16.4;  DB 8;  Length 33;
  Best Local Similarity   94.4%;  Pred. No. 6.4e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CCAGGCTAGCTACAACGA 24
              || |||||||||||||||
Db          7 CCTGGCTAGCTACAACGA 24


RESULT 14
US-11-056-620-18
; Sequence 18, Application US/11056620
; Publication No. US20060019914A1
; GENERAL INFORMATION:
;  APPLICANT: Pourmotabbed, Tayebeh
;  APPLICANT:  Hasegawa, Hisashi
;  APPLICANT:  Batson, Chad
;  TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND INVASION BY ANTI-MATRIX
;  TITLE OF INVENTION:  METALLOPROTEINASE DNAZYMES
;  FILE REFERENCE: 1306-22-2
;  CURRENT APPLICATION NUMBER: US/11/056,620
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: US 60/543,490
;  PRIOR FILING DATE: 2004-02-11
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
;   LENGTH: 33
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Negative control DNAzyme
US-11-056-620-18

  Query Match             49.7%;  Score 16.4;  DB 8;  Length 33;
  Best Local Similarity   94.4%;  Pred. No. 6.4e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CCAGGCTAGCTACAACGA 24
              | |||||||||||||||||
Db          7 CAAGGCTAGCTACAACGA 24


RESULT 15
US-11-056-620-23
; Sequence 23, Application US/11056620
; Publication No. US20060019914A1
; GENERAL INFORMATION:
;  APPLICANT: Pourmotabbed, Tayebeh
;  APPLICANT:  Hasegawa, Hisashi
;  APPLICANT:  Batson, Chad
;  TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND INVASION BY ANTI-MATRIX
;  TITLE OF INVENTION:  METALLOPROTEINASE DNAZYMES
```

; FILE REFERENCE: 1306-22-2
; CURRENT APPLICATION NUMBER: US/11/056,620
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,490
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: DNAzyme negative control
US-11-056-620-23

Query Match 49.7%; Score 16.4; DB 8; Length 33;
Best Local Similarity 94.4%; Pred. No. 6.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          7 CCAGGCTAGCTACAACGA 24
              | ||||||||||||||||
Db          7 CAAGGCTAGCTACAACGA 24
```

Search completed: February 4, 2006, 20:03:24
Job time : 308 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 18:20:27 ; Search time 2333 Seconds
(without alignments)
661.798 Million cell updates/sec

Title: US-09-889-075-6
Perfect score: 33
Sequence: 1 ccgcggccaggctagctacaacgacctggacga 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 67770

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13	39.4	24	9	BZ356735	BZ356735 SALK_1296
	2	12.8	38.8	27	9	AZ476237	AZ476237 1M0294A23
	3	12.6	38.2	29	8	D45817	D45817 HUMGS03036
c	4	12.4	37.6	29	6	CB842924	CB842924 M15E-3601
	5	12.4	37.6	29	9	AZ310073	AZ310073 1M0018H17
c	6	12.4	37.6	32	11	TA227H06Q	AL480011 T. brucei
	7	12.2	37.0	31	1	AA464328	AA464328 zx78e07.r
c	8	12	36.4	26	9	BH901408	BH901408 SALK_0790
c	9	12	36.4	28	10	CZ466185	CZ466185 c00081-3p
	10	12	36.4	31	9	AZ386571	AZ386571 1M0145C09
	11	12	36.4	32	10	AG204519	AG204519 Pan trogl
	12	12	36.4	33	2	BF026752	BF026752 601671969
	13	12	36.4	33	5	BQ584797	BQ584797 E011673-0
c	14	12	36.4	33	11	CR405193	CR405193 Arabidops
	15	11.8	35.8	25	9	AZ606311	AZ606311 1M0428G09
c	16	11.8	35.8	27	8	T97219	T97219 ye41e09.s1
c	17	11.8	35.8	29	9	AZ638368	AZ638368 1M0498A16
c	18	11.8	35.8	29	9	AZ767340	AZ767340 1M0566O22
	19	11.8	35.8	30	2	BE561270	BE561270 601344283
	20	11.8	35.8	30	9	AZ591789	AZ591789 1M0402P06
c	21	11.8	35.8	30	10	CZ443145	CZ443145 IBB9H12.r
c	22	11.8	35.8	30	10	CZ474258	CZ474258 d05010-5p
c	23	11.8	35.8	31	1	AA689463	AA689463 ns17h03.s
c	24	11.6	35.2	28	10	CZ477094	CZ477094 d10090-5p
	25	11.6	35.2	30	9	BH909028	BH909028 SALK_0517
c	26	11.6	35.2	32	10	CG726963	CG726963 1119092E0
c	27	11.4	34.5	25	9	BZ286303	BZ286303 KG08470-3
	28	11.4	34.5	25	10	AJ832265	AJ832265 Drosophil
	29	11.4	34.5	26	1	AJ747574	AJ747574 AJ747574
	30	11.4	34.5	26	9	BZ358021	BZ358021 SALK_1317
c	31	11.4	34.5	29	6	CB844212	CB844212 M15E-5164
	32	11.4	34.5	30	2	BE280898	BE280898 601155490
	33	11.4	34.5	30	2	BE559533	BE559533 601345383
	34	11.4	34.5	30	2	BE741581	BE741581 601594894
	35	11.4	34.5	31	1	AI434515	AI434515 ti45h11.x
	36	11.4	34.5	31	2	BE729154	BE729154 601561047
	37	11.4	34.5	31	3	BJ082844	BJ082844 BJ082844
	38	11.4	34.5	31	9	BH908618	BH908618 SALK_0496
c	39	11.4	34.5	32	1	AU257053	AU257053 AU257053
c	40	11.4	34.5	32	1	AV962684	AV962684 AV962684
	41	11.4	34.5	32	9	BZ592673	BZ592673 SALK_0284
	42	11.4	34.5	33	2	BE385013	BE385013 601276895
	43	11.2	33.9	20	9	AZ830894	AZ830894 2M0110E22
	44	11.2	33.9	25	9	AZ815986	AZ815986 2M0084H05
c	45	11.2	33.9	25	11	TA13E04Q	AL451474 T. brucei

ALIGNMENTS

RESULT 1
BZ356735
LOCUS BZ356735 24 bp DNA linear GSS 14-NOV-2002
DEFINITION SALK_129647.34.35.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_129647.34.35.x, genomic
survey sequence.
ACCESSION BZ356735
VERSION BZ356735.1 GI:24948377
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 24)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At5g38670.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1. .24
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_129647.34.35.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 39.4%; Score 13; DB 9; Length 24;
Best Local Similarity 76.2%; Pred. No. 1.3e+06;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy         13 TAGCTACAACGACCTGGACGA 33
              ||||  |||  |||| |||||
Db          1 TAGCAGCAAGAACCTTGACGA 21
```

RESULT 2
AZ476237
LOCUS AZ476237 27 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0294A23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0294A23 R, genomic survey sequence.
ACCESSION AZ476237
VERSION AZ476237.1 GI:10634362
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0294 row: A column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
FEATURES Location/Qualifiers
source 1. .27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0294A23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42.(gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 38.8%; Score 12.8; DB 9; Length 27;
Best Local Similarity 70.8%; Pred. No. 1.6e+06;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 CCGCGGCCAGGCTAGCTACAACGA 24
              ||  |||||||| || | ||  ||
Db          4 CCAGGGCCAGGCGAGGTGCAGGGA 27
```

RESULT 3
D45817
LOCUS D45817 29 bp mRNA linear EST 10-DEC-2003
DEFINITION HUMGS03036 Human adult lung 3' directed MboI cDNA Homo sapiens cDNA clone lg1181 3', mRNA sequence.
ACCESSION D45817
VERSION D45817.1 GI:662771
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 29)
AUTHORS Itoh,K., Okubo,K., Yosii,J., Yokouchi,H. and Matsubara,K.
TITLE An expression profile of active genes in human lung
JOURNAL DNA Res. 1, 279-287 (1994)
PUBMED 7719923
COMMENT Contact: Kohichi Itoh
Institute for Molecular and Cellular Biology
Osaka University
3-1, Yamadaoka, Suita, Osaka, 565, Japan
Tel: 06-877-5111 x3910
Fax: 06-877-1922
PROJECT = 'bodymapping'.
FEATURES Location/Qualifiers
source 1. .29
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="lg1181"
/dev_stage="adult"
/clone_lib="Human adult lung 3' directed MboI cDNA"
/note="Organ: lung; Adult human lung, 3' directed MboI"

ORIGIN

Query Match 38.2%; Score 12.6; DB 8; Length 29;
Best Local Similarity 78.9%; Pred. No. 1.9e+06;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 CCGCGGCCAGGCTAGCTAC 19
              ||||||| | | |||| |
Db         11 CCGCGGCCGGCCGAGCTGC 29
```

RESULT 4
CB842924/c
LOCUS CB842924 29 bp mRNA linear EST 25-AUG-2004
DEFINITION M15E-3601 MOUSE EMBRYONIC DAY 15.5 EYE Mus musculus cDNA 5', mRNA sequence.
ACCESSION CB842924
VERSION CB842924.2 GI:51550104
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Yu,J., Farjo,R., MacNee,S.P., Baehr,W., Stambolian,D.E. and Swaroop,A.

```
  TITLE     Annotation and analysis of 10,000 expressed sequence tags from
            developing mouse eye and adult retina
  JOURNAL   Genome Biol. 4 (10), R65 (2003)
   PUBMED   14519200
COMMENT     On Sep 1, 2003 this sequence version replaced gi:34374072.
            Contact: Swaroop, A.
            Department of Ophthalmology and Visual Sciences
            Kellogg Eye Center, University of Michigan
            540 KEC, 1000 Wall St., Ann Arbor, MI 48105, USA
            Tel: 734 615 2246
            Fax: 734 647 0228
            Email: swaroop@umich.edu.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="eye"
                     /clone_lib="MOUSE EMBRYONIC DAY 15.5 EYE"
                     /note="Vector: pSPORT1"
ORIGIN

  Query Match             37.6%;  Score 12.4;  DB 6;  Length 29;
  Best Local Similarity   72.7%;  Pred. No. 2.3e+06;
  Matches   16;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         11 GCTAGCTACAACGACCTGGACG 32
              || | ||| ||| | | |||||
Db         27 GCGATCTAGAACTATCCGGACG 6


RESULT 5
AZ310073
LOCUS       AZ310073                  29 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0018H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0018H17 R, genomic survey sequence.
ACCESSION   AZ310073
VERSION     AZ310073.1  GI:10351697
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000    Std Error: 0.00
            Plate: 0018  row: H  column: 17
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0018H17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             37.6%;  Score 12.4;  DB 9;  Length 29;
  Best Local Similarity   72.7%;  Pred. No. 2.3e+06;
  Matches   16;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 CGCGGCCAGGCTAGCTACAACG 23
              | | ||||||||||  || | |
Db          7 CTCTGCCAGGCTAGGGACTATG 28


RESULT 6
TA227H06Q/c
LOCUS       TA227H06Q                 32 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 227h06, reverse sequence,
            genomic survey sequence.
ACCESSION   AL480011
VERSION     AL480011.1  GI:11845938
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="227h06"
ORIGIN
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  Query Match            37.6%;  Score 12.4;  DB 11;  Length 32;
  Best Local Similarity  72.7%;  Pred. No. 2.3e+06;
  Matches   16;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         11 GCTAGCTACAACGACCTGGACG 32
              ||| ||| | ||||  || |||
Db         31 GCTCGCTTCCACGAAATGAACG 10


RESULT 7
AA464328
LOCUS       AA464328                 31 bp    mRNA    linear   EST 10-JUN-1997
DEFINITION  zx78e07.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:809892 5' similar to TR:G974284 G974284 SEMAPHORIN V. ;, mRNA
            sequence.
ACCESSION   AA464328
VERSION     AA464328.1  GI:2189212
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:6039740"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:809892"
                     /sex="Female"
                     /tissue_type="ovarian tumor"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares ovary tumor NbHOT"
                     /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. "
ORIGIN

  Query Match            37.0%;  Score 12.2;  DB 1;  Length 31;
  Best Local Similarity  68.0%;  Pred. No. 2.8e+06;
  Matches   17;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          5 GGCCAGGCTAGCTACAACGACCTGG 29
              ||||||    ||   |||||| |||
Db          5 GGCCAGATCTGCCGGAACGACGTGG 29


RESULT 8
BH901408/c
LOCUS       BH901408                 26 bp    DNA     linear   GSS 04-SEP-2002
DEFINITION  SALK_079024.36.15.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_079024.36.15.x, genomic
            survey sequence.
ACCESSION   BH901408
VERSION     BH901408.1  GI:22712289
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_079024.36.15.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match            36.4%;  Score 12;  DB 9;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 3.4e+06;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGCTAGCTACAA 21
              ||||||||||||
Db         21 GGCTAGCTACAA 10


RESULT 9
CZ466185/c
LOCUS       CZ466185                 28 bp    DNA     linear   GSS 29-APR-2005
DEFINITION  c00081-3prime Exelixis piggyBac PB insertions Drosophila
            melanogaster genomic Sequence recovered from 3' end of piggyBac,
            genomic survey sequence.
ACCESSION   CZ466185
VERSION     CZ466185.1  GI:62960198
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
```

```
            Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
            Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
            Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
            Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
            Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
            Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.L. and Margolis,J.
  TITLE     A complementary transposon tool kit for Drosophila melanogaster
            using P and piggyBac
  JOURNAL   Nat. Genet. 36 (3), 283-287 (2004)
   PUBMED   14981521
COMMENT     Contact: Roger A Hoskins
            Berkeley Drosophila Genome Project
            Lawrence Berkeley National Laboratory
            Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
            Tel: 510 486 4015
            Fax: 510 486 6798
            Email: RHoskins@lbl.gov
            Sequence recovery method was inverse PCR.
            Sequence orientation is forward strand relative to 5' end of
            piggyBac element.
            The piggyBac insertion position is 1 in the 28 bases. This
            insertion position refers to the first base of the 4 base TTAA
            target recognition sequence.
            Class: transposon insertion site.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /strain="isogenic w- strain"
                     /db_xref="taxon:7227"
                     /clone_lib="Exelixis piggyBac PB insertions"
                     /note="Vector: piggyBac PB (GenBank accession number
                     AY515146); An isogenic w- Drosophila melanogaster strain
                     was mutagenized by remobilization of transposable
                     elements. We remobilized the PB element using
                     Hsp70:piggyBac transposase from a single ammunition
                     element on either the X or third chromosome. We induced
                     transposase expression by immersing bottles in a
                     circulating 37oC water bath for a daily (days 3-10 after
                     egg-laying) 1-h heat shock. We outcrossed the resulting
                     dysgenic males to an isogenic w- strain. New insertions
                     were identified on the basis of a change in eye color
                     (third chromosome ammunition) or the appearance of w+ male
                     progeny (X chromosome ammunition). All lines were mapped
                     to a chromosome by standard genetic methods, examined for
                     homozygous viability, and used for recovery of flanking
                     genomic sequence by inverse PCR."
ORIGIN

  Query Match           36.4%;  Score 12;  DB 10;  Length 28;
  Best Local Similarity   75.0%;  Pred. No. 3.4e+06;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          6 GCCAGGCTAGCTACAACGAC 25
              ||  || | |||||||| ||
Db         28 GCGCGGTTCGCTACAACAAC 9


RESULT 10
AZ386571
LOCUS       AZ386571                 31 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0145C09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0145C09 R, genomic survey sequence.
ACCESSION   AZ386571
VERSION     AZ386571.1  GI:10500271
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0145  row: C  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0145C09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match           36.4%;  Score 12;  DB 9;  Length 31;
  Best Local Similarity   75.0%;  Pred. No. 3.4e+06;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         10 GGCTAGCTACAACGACCTGG 29
              |||||||| | |  || ||
Db         10 GGCTAGCTATACCTTCCAGG 29


RESULT 11
AG204519
LOCUS       AG204519                 32 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-090C09.T7, genomic survey
            sequence.
ACCESSION   AG204519
VERSION     AG204519.1  GI:45236694
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1
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  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 32)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                Sequencing: T7
             LIBRARY
                Vector    : pBACe3.6
                R.Site 1  : EcoRI
                R.Site 2  : EcoRI.
FEATURES              Location/Qualifiers
     source           1. .32
                      /organism="Pan troglodytes"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9598"
                      /clone="RP43-090C09.T7"
                      /sex="male"
                      /cell_type="lymphocytes"
                      /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match           36.4%;  Score 12;  DB 10;  Length 32;
  Best Local Similarity  75.0%;  Pred. No. 3.4e+06;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          8 CAGGCTAGCTACAACGACCT 27
              ||||||| |||  ||  |||
Db          9 CAGGCTATCTATTACTGCCT 28


RESULT 12
BF026752
LOCUS       BF026752                  33 bp    mRNA    linear   EST 10-OCT-2000
DEFINITION  601671969F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954905 5',
            mRNA sequence.
ACCESSION   BF026752
VERSION     BF026752.1  GI:10734464
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM828  row: i  column: 18.
FEATURES              Location/Qualifiers
     source           1. .33
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:3954905"
                      /tissue_type="melanotic melanoma"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_20"
                      /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match           36.4%;  Score 12;  DB 2;  Length 33;
  Best Local Similarity  75.0%;  Pred. No. 3.4e+06;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         10 GGCTAGCTACAACGACCTGG 29
              ||||||  | | | | |||||
Db          7 GGCTAGGTGCGAGGCCCTGG 26


RESULT 13
BQ584797
LOCUS       BQ584797                  33 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E011673-024-002-O13-SP6R MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-002-O13 5-PRIME, mRNA sequence.
ACCESSION   BQ584797
VERSION     BQ584797.1  GI:26114374
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 33   Std Error: 0.00
            Plate: 2  row: O  column: 13
            Seq primer: SP6r; ATTTAGGTGACACTATAGAAGA.
FEATURES              Location/Qualifiers
     source           1. .33
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:181910"
                      /db_xref="taxon:161934"
                      /clone="024-002-O13"
                      /tissue_type="inflorescence"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-inflorescence"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
```

Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN

Query Match 36.4%; Score 12; DB 5; Length 33;
Best Local Similarity 64.3%; Pred. No. 3.4e+06;
Matches 18; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
Qy          3 GCGGCCAGGCTAGCTACAACGACCTGGA 30
              || || |   ||| |||||   |||||
Db          2 GCTGCTAATGAAGCCACAACTGACTGGA 29
```

RESULT 14
CR405193/c
LOCUS CR405193 33 bp DNA linear GSS 02-MAY-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-876E02-026468, genomic survey sequence.
ACCESSION CR405193
VERSION CR405193.1 GI:46945921
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Li,Y., Rosso;M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 33)
AUTHORS Li,Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5g22250. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES Location/Qualifiers
source 1. .33
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-876E02-026468"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
ORIGIN

Query Match 36.4%; Score 12; DB 11; Length 33;
Best Local Similarity 75.0%; Pred. No. 3.4e+06;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy         13 TAGCTACAACGACCTGGACG 32
              ||  |||||||||  || | |
Db         25 TAAATACAACGACTTGAATG 6
```

RESULT 15
AZ606311
LOCUS AZ606311 25 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0428G09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0428G09 F, genomic survey sequence.
ACCESSION AZ606311
VERSION AZ606311.1 GI:11728501
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0428 row: G column: 09
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
FEATURES Location/Qualifiers
source 1. .25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0428G09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN

Query Match 35.8%; Score 11.8; DB 9; Length 25;
Best Local Similarity 69.6%; Pred. No. 4e+06;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy          2 CGCGGCCAGGCTAGCTACAACGA 24
              ||||||| |  | ||  | ||||
Db          2 CGCGGCCGGAGTGGCCCCGACGA 24
```

Search completed: February 4, 2006, 19:47:23
Job time : 2338 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 16:36:24 ; Search time 313 Seconds
(without alignments)
702.667 Million cell updates/sec

Title: US-09-889-075-6
Perfect score: 33
Sequence: 1 ccgcggccaggctagctacaacgacctggacga 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4337854

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	33	100.0	33	3	AAA74390	Aaa74390 Human Egr
2	33	100.0	33	4	AAF85125	Aaf85125 Nucleotid
3	28.8	87.3	33	3	AAA74391	Aaa74391 Human Egr
4	28.8	87.3	33	4	AAF85126	Aaf85126 Nucleotid
5	25.8	78.2	31	6	ACN33570	Acn33570 WNV minus
6	25.4	77.0	31	8	ABZ64054	Abz64054 Human H-R
7	25.4	77.0	31	14	ADZ33128	Adz33128 Human H-R
8	25.2	76.4	31	5	ADV06670	Adv06670 Human BAC
9	24.8	75.2	31	6	ACN33534	Acn33534 WNV minus
10	24.6	74.5	31	4	ABK06338	Abk06338 Human NOG
11	24.6	74.5	31	8	ABZ62232	Abz62232 Human K-R
12	24.6	74.5	31	14	ADZ31306	Adz31306 Human K-R
13	24.2	73.3	31	11	ADL52905	Adl52905 Human NOG
14	24	72.7	31	8	ACD60105	Acd60105 HCV DNAzy
15	24	72.7	31	8	ACD59680	Acd59680 HCV DNAzy
16	24	72.7	31	12	ADI88977	Adi88977 HCV DNAzy
17	24	72.7	31	12	ADI89178	Adi89178 HCV DNAzy
18	23.8	72.1	31	11	AEB60264	Aeb60264 Human VEG
19	23.8	72.1	33	8	ABT16701	Abt16701 bcl-xL DN
20	23.6	71.5	31	4	ABL48084	Abl48084 Human GRI
21	23.6	71.5	31	6	ACN34140	Acn34140 WNV minus
22	23.6	71.5	31	8	ABZ65537	Abz65537 Human HER
23	23.6	71.5	31	8	ABZ64419	Abz64419 Human H-R
24	23.6	71.5	31	11	ADL75905	Adl75905 Human PTG
25	23.6	71.5	31	11	ADM55369	Adm55369 DNAzyme t
26	23.6	71.5	31	14	ADZ33493	Adz33493 Human H-R
27	23.6	71.5	31	14	ADZ34611	Adz34611 Human HER
28	23.6	71.5	33	8	ABT16677	Abt16677 bcl-2 DNA
29	23.6	71.5	33	14	ADZ39662	Adz39662 Human GAT
30	23.4	70.9	31	5	ADV06566	Adv06566 Human BAC
31	23.4	70.9	31	6	ACN33574	Acn33574 WNV minus
32	23.4	70.9	31	8	ABZ65862	Abz65862 Human HER
33	23.4	70.9	31	8	ACD64769	Acd64769 HCV minus
34	23.4	70.9	31	8	ACD59318	Acd59318 HCV DNAzy
35	23.4	70.9	31	12	ADI88783	Adi88783 HCV DNAzy
36	23.4	70.9	31	14	ADZ34936	Adz34936 Human HER
37	23.4	70.9	33	4	AAD11883	Aad11883 Therapeut
38	23.4	70.9	33	10	ADF93240	Adf93240 VEGF-rela
39	23.2	70.3	31	6	ACN21290	Acn21290 WNV DNAzy
40	23.2	70.3	31	6	ACN33189	Acn33189 WNV minus
41	23.2	70.3	31	8	ACD56893	Acd56893 HCV DNAzy
42	23.2	70.3	31	11	AEB59721	Aeb59721 Human VEG
43	23.2	70.3	31	12	ADI87348	Adi87348 HCV DNAzy
44	23.2	70.3	33	14	ADZ39706	Adz39706 Human GAT
45	23.2	70.3	33	14	ADZ39717	Adz39717 Human T-b

ALIGNMENTS

RESULT 1
AAA74390
ID AAA74390 standard; DNA; 33 BP.
XX
AC AAA74390;
XX
DT 30-NOV-2000 (first entry)
XX
DE Human Egr-1 DNAzyme #4.
XX
KW Human; Egr-1; NGFI-A; transcription factor; DNAzyme;
KW vascular smooth muscle cell; post-angioplasty restenosis;
KW vein graft failure; transplant coronary disease; atherosclerosis;
KW cerebrovascular infarction; stroke; myocardial; heart attack;
KW hypertension; peripheral vascular; gangrene; neoplasia; ss.
XX
OS Homo sapiens.
XX
PN WO200042173-A1.
XX
PD 20-JUL-2000.
XX
PF 11-JAN-2000; 2000WO-AU000011.
XX
PR 11-JAN-1999; 99AU-00008103.
XX
PA (UNIX) UNISEARCH LTD.
PA (JOHJ) JOHNSON & JOHNSON RES PTY LTD.
XX
PI Atkins DG, Baker AR, Khachigian LM;
XX
DR WPI; 2000-476054/41.
XX
PT DNAzyme for treating conditions associated with proliferation or
PT migration of cells e.g. post-angioplasty restenosis, vein graft failure
PT and hypertension cleaves mRNA molecules encoding EGR-1.
XX
PS Claim 6; Page 9; 62pp; English.
XX
CC Egr-1 (also known as EGR-1 and NGFI-A) is a transcription factor. Egr-1
CC binds to the promoters of genes whose products influence cell movement
CC and replication in the artery wall. DNA-based enzymes (DNAzymes), have

CC been developed in the present invention, which can cut Egr-1 mRNA with
CC high efficiency and specificity, resulting in Egr-1 activity inhibition
CC in vascular smooth muscle cells. The present sequence is one such Egr-1
CC specific DNAzyme. The DNAzyme can be used to inhibit EGR-1 activity in
CC cells, inhibit proliferation or migration of cells and to treat a
CC condition associated with cell proliferation or migration e.g. post-
CC angioplasty restenosis, vein graft failure, transplant coronary disease
CC and complications associated with atherosclerosis e.g. cerebrovascular
CC infarction (stroke), myocardial infarction (heart attack), hypertension
CC or peripheral vascular disease e.g. gangrene of the extremities. The
CC cells which are treated are vascular cells, preferably smooth muscle or
CC endothelial cells or cells involved in neoplasia
XX
SQ Sequence 33 BP; 8 A; 12 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 33; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGCGGCCAGGCTAGCTACAACGACCTGGACGA 33
              |||||||||||||||||||||||||||||||||
Db          1 CCGCGGCCAGGCTAGCTACAACGACCTGGACGA 33
```

RESULT 2
AAF85125
ID AAF85125 standard; DNA; 33 BP.
XX
AC AAF85125;
XX
DT 09-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a DNAzyme which targets an EGR gene.
XX
KW Early growth response factor; EGR; tumour cell; tumour; DNAzyme;
KW antisense oligonucleotide; prostate tumour; hepatocellular carcinoma;
KW skin carcinoma; breast tumour; ss.
XX
OS Synthetic.
XX
PN WO200130394-A1.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-AU001315.
XX
PR 26-OCT-1999; 99AU-00003676.
XX
PA (UNIX) UNISEARCH LTD.
XX
PI Khachigian LM;
XX
DR WPI; 2001-300428/31.
XX
PT Treating tumors including prostate tumor, breast tumor, skin carcinoma,
PT comprises administering agent which inhibits induction or decreases
PT expression of early growth response factor-1.
XX
PS Claim 18; Page 50; 80pp; English.
XX
CC The present sequence represents a DNAzyme, which cleaves an early growth
CC response factor (EGR) gene. The specification describes a method for
CC inhibiting the growth or proliferation of a tumour cell and treating
CC tumours. The method comprises contacting a tumour cell or administering
CC to a subject, an agent which inhibits induction, decreases expression or
CC which decreases the nuclear accumulation or activity of EGR. The agent is
CC a DNAzyme or an antisense oligonucleotide. The method is useful for
CC treating solid tumours, including prostate tumours, hepatocellular
CC carcinoma, skin carcinoma or breast tumours
XX
SQ Sequence 33 BP; 8 A; 12 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 33; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGCGGCCAGGCTAGCTACAACGACCTGGACGA 33
              |||||||||||||||||||||||||||||||||
Db          1 CCGCGGCCAGGCTAGCTACAACGACCTGGACGA 33
```

RESULT 3
AAA74391
ID AAA74391 standard; DNA; 33 BP.
XX
AC AAA74391;
XX
DT 30-NOV-2000 (first entry)
XX
DE Human Egr-1 DNAzyme #5.
XX
KW Human; Egr-1; NGFI-A; transcription factor; DNAzyme;
KW vascular smooth muscle cell; post-angioplasty restenosis;
KW vein graft failure; transplant coronary disease; atherosclerosis;
KW cerebrovascular infarction; stroke; myocardial; heart attack;
KW hypertension; peripheral vascular; gangrene; neoplasia; ss.
XX
OS Homo sapiens.
XX
PN WO200042173-A1.
XX
PD 20-JUL-2000.
XX
PF 11-JAN-2000; 2000WO-AU000011.
XX
PR 11-JAN-1999; 99AU-00008103.
XX
PA (UNIX) UNISEARCH LTD.
PA (JOHJ) JOHNSON & JOHNSON RES PTY LTD.
XX
PI Atkins DG, Baker AR, Khachigian LM;
XX
DR WPI; 2000-476054/41.
XX
PT DNAzyme for treating conditions associated with proliferation or
PT migration of cells e.g. post-angioplasty restenosis, vein graft failure
PT and hypertension cleaves mRNA molecules encoding EGR-1.
XX
PS Claim 6; Page 9; 62pp; English.
XX
CC Egr-1 (also known as EGR-1 and NGFI-A) is a transcription factor. Egr-1
CC binds to the promoters of genes whose products influence cell movement
CC and replication in the artery wall. DNA-based enzymes (DNAzymes), have
CC been developed in the present invention, which can cut Egr-1 mRNA with
CC high efficiency and specificity, resulting in Egr-1 activity inhibition
CC in vascular smooth muscle cells. The present sequence is one such Egr-1
CC specific DNAzyme. The DNAzyme can be used to inhibit EGR-1 activity in
CC cells, inhibit proliferation or migration of cells and to treat a
CC condition associated with cell proliferation or migration e.g. post-
CC angioplasty restenosis, vein graft failure, transplant coronary disease
CC and complications associated with atherosclerosis e.g. cerebrovascular
CC infarction (stroke), myocardial infarction (heart attack), hypertension
CC or peripheral vascular disease e.g. gangrene of the extremities. The
CC cells which are treated are vascular cells, preferably smooth muscle or
CC endothelial cells or cells involved in neoplasia
XX
SQ Sequence 33 BP; 7 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 87.3%; Score 28.8; DB 3; Length 33;
Best Local Similarity 93.8%; Pred. No. 0.078;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 CCGCGGCCAGGCTAGCTACAACGACCTGGACG 32
              |||| ||||||||||||||||||||| |||||
Db          1 CCGCTGCCAGGCTAGCTACAACGACCCGGACG 32
```

RESULT 4
AAF85126
ID AAF85126 standard; DNA; 33 BP.
XX
AC AAF85126;
XX
DT 09-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a DNAzyme which targets an EGR gene.
XX
KW Early growth response factor; EGR; tumour cell; tumour; DNAzyme;
KW antisense oligonucleotide; prostate tumour; hepatocellular carcinoma;
KW skin carcinoma; breast tumour; ss.
XX
OS Synthetic.
XX
PN WO200130394-A1.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-AU001315.
XX
PR 26-OCT-1999; 99AU-00003676.
XX
PA (UNIX) UNISEARCH LTD.
XX
PI Khachigian LM;
XX
DR WPI; 2001-300428/31.
XX
PT Treating tumors including prostate tumor, breast tumor, skin carcinoma,
PT comprises administering agent which inhibits induction or decreases
PT expression of early growth response factor-1.
XX
PS Claim 18; Page 50; 80pp; English.
XX
CC The present sequence represents a DNAzyme, which cleaves an early growth
CC response factor (EGR) gene. The specification describes a method for
CC inhibiting the growth or proliferation of a tumour cell and treating
CC tumours. The method comprises contacting a tumour cell or administering
CC to a subject, an agent which inhibits induction, decreases expression or
CC which decreases the nuclear accumulation or activity of EGR. The agent is
CC a DNAzyme or an antisense oligonucleotide. The method is useful for
CC treating solid tumours, including prostate tumours, hepatocellular
CC carcinoma, skin carcinoma or breast tumours
XX
SQ Sequence 33 BP; 7 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 87.3%; Score 28.8; DB 4; Length 33;
Best Local Similarity 93.8%; Pred. No. 0.078;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGCGGCCAGGCTAGCTACAACGACCTGGACG 32
|||| |||||||||||||||||||| |||||
Db 1 CCGCTGCCAGGCTAGCTACAACGACCCGGACG 32

RESULT 5
ACN33570
ID ACN33570 standard; RNA; 31 BP.
XX
AC ACN33570;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV minus strand DNAzyme SEQ ID NO 33586.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 24; SEQ ID NO 33586; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 31 BP; 8 A; 9 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 78.2%; Score 25.8; DB 6; Length 31;
Best Local Similarity 93.1%; Pred. No. 1.2;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCGGCCAGGCTAGCTACAACGACCTGGAC 31
|||| |||||||||||||||||| |||||
Db 2 GCGGACAGGCTAGCTACAACGACGTGGAC 30

RESULT 6
ABZ64054
ID ABZ64054 standard; RNA; 31 BP.
XX
AC ABZ64054;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human H-Ras DNAzyme #517.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX

PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 65; Page 121; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519, ABZ66525 - ABZ66529,
CC ABZ66586 - ABZ66658 represent human ribozymes of the invention
XX
SQ Sequence 31 BP; 6 A; 9 C; 13 G; 3 T; 0 U; 0 Other;

Query Match 77.0%; Score 25.4; DB 8; Length 31;
Best Local Similarity 96.3%; Pred. No. 1.8;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGGCCAGGCTAGCTACAACGACCTGG 29
||||||||||||||||||||||||||||
Db 2 GCGGCCGGGCTAGCTACAACGACCTGG 28

RESULT 7
ADZ33128
ID ADZ33128 standard; DNA; 31 BP.
XX
AC ADZ33128;
XX
DT 30-JUN-2005 (first entry)
XX
DE Human H-Ras DNAzyme sequence SEQ ID NO:4166.
XX
KW short interfering RNA; siRNA; RNA interference; gene silencing;
KW cytostatic; cancer; Ras gene; ribozyme; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2005080031-A1.
XX
PD 14-APR-2005.
XX
PF 26-NOV-2003; 2003US-00724270.
XX
PR 18-MAY-2001; 2001US-0292217P.
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 20-JUL-2001; 2001US-0306883P.
PR 13-AUG-2001; 2001US-0311865P.
PR 10-SEP-2001; 2001US-0318471P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.
PR 20-MAY-2002; 2002WO-US015876.
PR 29-MAY-2002; 2002US-00157580.
PR 29-MAY-2002; 2002WO-US016840.
PR 06-JUN-2002; 2002US-00163552.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 10-SEP-2002; 2002US-00238700.
PR 15-JAN-2003; 2003US-0440129P.
PR 20-FEB-2003; 2003WO-US005028.
PR 20-FEB-2003; 2003WO-US005346.
PR 16-APR-2003; 2003US-00417012.
PR 24-APR-2003; 2003US-00422704.
PR 30-APR-2003; 2003US-00427160.
PR 23-MAY-2003; 2003US-00444853.
PR 29-AUG-2003; 2003US-00652791.
PR 23-OCT-2003; 2003US-00693059.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2005-331166/34.
XX
PT Novel double-stranded short interfering RNA molecule having first
PT nucleotide sequence complementary to RNA encoding HER2 or its portion,
PT and second nucleotide sequence having complementarity to first sequence,
PT useful for treating cancer.
XX
PS Example 1; SEQ ID NO 4166; 143pp; English.
XX
CC The invention relates to a double-stranded short interfering RNA (siRNA)
CC molecule (I) comprising a first nucleotide sequence having 19-23
CC nucleotides complementary to an RNA sequence encoding HER2 or its
CC portion, and a second nucleotide sequence having 19-23 nucleotides
CC exhibiting complementarity to the first sequence, and including at least
CC one nucleotide that is not a 2'-OH containing ribonucleotide. Also
CC described is a method of producing a class of nucleic acid-based gene
CC modulating agents that exhibit a high degree of specificity for RNA of a
CC desired target. (I) is useful for modulating HER2 activity in a cell, and
CC for treating diseases or conditions related to levels of HER2 gene
CC expression. (I) is useful for treating cancer, such as pancreatic cancer,
CC bladder cancer, lung cancer, breast cancer or prostrate cancer. The
CC present sequence represents a human H-Ras DNAzyme (ribozyme), which is
CC used in an example from the present invention for the identification of
CC potential target sites in human Ras RNA.
XX
SQ Sequence 31 BP; 6 A; 9 C; 13 G; 3 T; 0 U; 0 Other;

Query Match 77.0%; Score 25.4; DB 14; Length 31;
Best Local Similarity 96.3%; Pred. No. 1.8;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGGCCAGGCTAGCTACAACGACCTGG 29
||||||||||||||||||||||||||||
Db 2 GCGGCCGGGCTAGCTACAACGACCTGG 28

RESULT 8
ADV06670
ID ADV06670 standard; DNA; 31 BP.
XX
AC ADV06670;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human BACE DNAzyme sequence #528.
XX
KW Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;

KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ds.
XX
OS Homo sapiens.
XX
PN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX
DR WPI; 2001-244406/25.
XX
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
PT obesity and heart disease.
XX
PS Example 4; Page 387; 717pp; English.
XX
CC The present invention relates to the use of enzymatic nucleic acid
CC molecules (e.g. ribozymes) to modulate gene expression. The invention
CC also methods for their use to down regulate or inhibit the expression of
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
CC zinzyme, and/or DNAzyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a DNAzyme used in the examples of the present
CC invention. Note: Some SEQ ID Nos are repeated more than once in the
CC specification, but these have different sequences associated with them.
XX
SQ Sequence 31 BP; 7 A; 11 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 76.4%; Score 25.2; DB 5; Length 31;
Best Local Similarity 90.0%; Pred. No. 2.1;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGAC 31
              ||| ||| ||||||||||||||||||| ||
Db          1 CGCTGCCGGGCTAGCTACAACGACCTGAAC 30
```

RESULT 9
ACN33534
ID ACN33534 standard; RNA; 31 BP.
XX
AC ACN33534;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV minus strand DNAzyme SEQ ID NO 33550.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 24; SEQ ID NO 33550; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 31 BP; 8 A; 9 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 75.2%; Score 24.8; DB 6; Length 31;
Best Local Similarity 92.9%; Pred. No. 3.1;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 GGCCAGGCTAGCTACAACGACCTGGACG 32
              |||||||||||||||||||| ||| |
Db          4 GGCCAGGCTAGCTACAACGACCAGGAGG 31
```

RESULT 10
ABK06338
ID ABK06338 standard; DNA; 31 BP.
XX
AC ABK06338;
XX
DT 12-MAR-2002 (first entry)

XX
DE Human NOGO DNAzyme substrate sequence #351.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004273.
XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX
DR WPI; 2001-607195/69.
XX
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 89; Page 108; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg^2^+.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targetting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg^2^+. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a substrate sequence for a nucleic acid of the invention
CC based on the human NOGO sequence
XX
SQ Sequence 31 BP; 7 A; 9 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 74.5%; Score 24.6; DB 4; Length 31;
Best Local Similarity 87.1%; Pred. No. 3.7;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGCGGCCAGGCTAGCTACAACGACCTGGACG 32
||||| |||||||||||||||.||| | ||||
Db 1 CGCGGGCAGGCTAGCTACAACGAGGTCGACG 31

RESULT 11
ABZ62232
ID ABZ62232 standard; RNA; 31 BP.
XX
AC ABZ62232;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human K-Ras DNAzyme #16.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 65; Page 85; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ62217 - ABZ64543, ABZ65532 - ABZ65519, ABZ66525 - ABZ66529,
CC ABZ66586 - ABZ66658 represent human ribozymes of the invention
XX
SQ Sequence 31 BP; 6 A; 13 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 74.5%; Score 24.6; DB 8; Length 31;
Best Local Similarity 87.1%; Pred. No. 3.7;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGCGGCCAGGCTAGCTACAACGACCTGGACG 32

```
                ||| |||||||||||||||||||| | | ||
Db          1 CGCCGCCAGGCTAGCTACAACGACTTCGCCG 31
```

RESULT 12
ADZ31306
ID ADZ31306 standard; DNA; 31 BP.
XX
AC ADZ31306;
XX
DT 30-JUN-2005 (first entry)
XX
DE Human K-Ras DNAzyme sequence SEQ ID NO:2344.
XX
KW short interfering RNA; siRNA; RNA interference; gene silencing;
KW cytostatic; cancer; Ras gene; ribozyme; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2005080031-A1.
XX
PD 14-APR-2005.
XX
PF 26-NOV-2003; 2003US-00724270.
XX
PR 18-MAY-2001; 2001US-0292217P.
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 20-JUL-2001; 2001US-0306883P.
PR 13-AUG-2001; 2001US-0311865P.
PR 10-SEP-2001; 2001US-0318471P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.
PR 20-MAY-2002; 2002WO-US015876.
PR 29-MAY-2002; 2002US-00157580.
PR 29-MAY-2002; 2002WO-US016840.
PR 06-JUN-2002; 2002US-00163552.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 10-SEP-2002; 2002US-00238700.
PR 15-JAN-2003; 2003US-0440129P.
PR 20-FEB-2003; 2003WO-US005028.
PR 20-FEB-2003; 2003WO-US005346.
PR 16-APR-2003; 2003US-00417012.
PR 24-APR-2003; 2003US-00422704.
PR 30-APR-2003; 2003US-00427160.
PR 23-MAY-2003; 2003US-00444853.
PR 29-AUG-2003; 2003US-00652791.
PR 23-OCT-2003; 2003US-00693059.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2005-331166/34.
XX
PT Novel double-stranded short interfering RNA molecule having first
PT nucleotide sequence complementary to RNA encoding HER2 or its portion,
PT and second nucleotide sequence having complementarity to first sequence,
PT useful for treating cancer.
XX
PS Example 1; SEQ ID NO 2344; 143pp; English.
XX
CC The invention relates to a double-stranded short interfering RNA (siRNA)
CC molecule (I) comprising a first nucleotide sequence having 19-23
CC nucleotides complementary to an RNA sequence encoding HER2 or its
CC portion, and a second nucleotide sequence having 19-23 nucleotides
CC exhibiting complementarity to the first sequence, and including at least
CC one nucleotide that is not a 2'-OH containing ribonucleotide. Also
CC described is a method of producing a class of nucleic acid-based gene
CC modulating agents that exhibit a high degree of specificity for RNA of a
CC desired target. (I) is useful for modulating HER2 activity in a cell, and
CC for treating diseases or conditions related to levels of HER2 gene
CC expression. (I) is useful for treating cancer, such as pancreatic cancer,
CC bladder cancer, lung cancer, breast cancer or prostrate cancer. The
CC present sequence represents a human K-Ras DNAzyme (ribozyme), which is
CC used in an example from the present invention for the identification of
CC potential target sites in human Ras RNA.
XX
SQ Sequence 31 BP; 6 A; 13 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match   74.5%; Score 24.6; DB 14; Length 31;
  Best Local Similarity   87.1%; Pred. No. 3.7;
  Matches   27; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

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Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGACG 32
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Db          1 CGCCGCCAGGCTAGCTACAACGACTTCGCCG 31
```

RESULT 13
ADL52905
ID ADL52905 standard; RNA; 31 BP.
XX
AC ADL52905;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human NOGO receptor DNAzyme sequence #66.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis;
KW NOGO receptor DNAzyme; substrate; ss; human.
XX
OS Homo sapiens.
XX
PN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haeberli P, Mcswiggen J, Fosnaugh K;
XX
DR WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 7; SEQ ID NO 6438; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,

```
CC   restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC   disease, lupus, multiple sclerosis, transplant/graft rejection,
CC   ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC   conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC   nucleic acids of the invention are also useful for down-regulating the
CC   expression of a target gene and as a diagnostic tool to examine genetic
CC   drifts and mutations within diseased cells or to detect the presence of a
CC   target RNA in a cell. The present RNA sequence represents a human NOGO
CC   receptor DNAzyme sequence.
XX
SQ   Sequence 31 BP; 8 A; 8 C; 11 G; 4 T; 0 U; 0 Other;

  Query Match             73.3%;  Score 24.2;  DB 11;  Length 31;
  Best Local Similarity   89.7%;  Pred. No. 5.3;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGA 30
              | ||| |||||||||||||||||| |||||
Db          1 CTCGGGCAGGCTAGCTACAACGAGCTGGA 29


RESULT 14
ACD60105
ID   ACD60105 standard; DNA; 31 BP.
XX
AC   ACD60105;
XX
DT   24-SEP-2003  (first entry)
XX
DE   HCV DNAzyme sequence #1627.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Claim 1; Page 263; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents one of the HCV DNAzyme or
CC   minus strand DNAzyme sequences disclosed in the present invention
XX
SQ   Sequence 31 BP; 9 A; 11 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             72.7%;  Score 24;  DB 8;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 6.4;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCGGCCAGGCTAGCTACAACGACC 26
              ||||||||||||||||||||||||
Db          2 GCGGCCAGGCTAGCTACAACGACC 25


RESULT 15
ACD59680
ID   ACD59680 standard; DNA; 31 BP.
XX
AC   ACD59680;
XX
DT   24-SEP-2003  (first entry)
XX
DE   HCV DNAzyme sequence #1426.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
```

XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Claim 1; Page 259; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents one of the HCV DNAzyme or
CC minus strand DNAzyme sequences disclosed in the present invention
XX
SQ Sequence 31 BP; 7 A; 13 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 72.7%; Score 24; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCGGCCAGGCTAGCTACAACGACC 26
||||||||||||||||||||||||
Db 2 GCGGCCAGGCTAGCTACAACGACC 25

Search completed: February 4, 2006, 18:39:20
Job time : 316 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 18:18:38 ; Search time 1732 Seconds
(without alignments)
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Title: US-09-889-075-6
Perfect score: 33
Sequence: 1 ccgcggccaggctagctacaacgacctggacga 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1731194

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_in:*
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6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	33	100.0	33	6	BD242794	BD242794 Catalytic
2	28.8	87.3	33	6	BD242795	BD242795 Catalytic
3	24.6	74.5	31	6	AX220896	AX220896 Sequence
4	23.6	71.5	31	6	AX274148	AX274148 Sequence
5	23.6	71.5	33	6	CS075086	CS075086 Sequence
6	23.2	70.3	33	6	CS075130	CS075130 Sequence
7	23.2	70.3	33	6	CS075141	CS075141 Sequence
8	23	69.7	31	6	AX220857	AX220857 Sequence
9	22.8	69.1	31	6	AX274253	AX274253 Sequence
10	22.8	69.1	31	6	AX425682	AX425682 Sequence
11	22.8	69.1	33	6	CS075117	CS075117 Sequence
12	22.8	69.1	33	6	CS075118	CS075118 Sequence
13	22.4	67.9	31	6	AX426000	AX426000 Sequence
14	22.4	67.9	33	6	CS075168	CS075168 Sequence
15	22.2	67.3	31	6	AX426030	AX426030 Sequence
16	22.2	67.3	33	6	CS075149	CS075149 Sequence
17	22	66.7	31	6	E44266	E44266 Oligo-DNA s
18	22	66.7	31	6	AX220905	AX220905 Sequence
19	22	66.7	31	6	AX425982	AX425982 Sequence
20	22	66.7	31	6	AX426005	AX426005 Sequence
21	22	66.7	33	6	CS075169	CS075169 Sequence
22	21.8	66.1	31	6	AX221330	AX221330 Sequence
23	21.8	66.1	31	6	AX425783	AX425783 Sequence
24	21.8	66.1	31	6	AX425823	AX425823 Sequence
25	21.8	66.1	31	6	AX582470	AX582470 Sequence
26	21.8	66.1	31	6	AX582732	AX582732 Sequence
27	21.8	66.1	33	6	CS075083	CS075083 Sequence
28	21.8	66.1	33	6	CS075179	CS075179 Sequence
29	21.6	65.5	31	6	AX221169	AX221169 Sequence
30	21.6	65.5	31	6	AX221378	AX221378 Sequence
31	21.6	65.5	31	6	AX274060	AX274060 Sequence
32	21.6	65.5	31	6	AX425860	AX425860 Sequence
33	21.6	65.5	31	6	AX426059	AX426059 Sequence
34	21.6	65.5	31	6	AX582316	AX582316 Sequence
35	21.6	65.5	31	6	AX582709	AX582709 Sequence
36	21.6	65.5	31	6	AX582719	AX582719 Sequence
37	21.6	65.5	33	6	CS075069	CS075069 Sequence
38	21.4	64.8	31	6	AX425980	AX425980 Sequence
39	21.4	64.8	31	6	AX582510	AX582510 Sequence
40	21.4	64.8	33	6	CS075121	CS075121 Sequence
41	21.4	64.8	33	6	CS075147	CS075147 Sequence
42	21.2	64.2	31	6	AX221331	AX221331 Sequence
43	21.2	64.2	31	6	AX274025	AX274025 Sequence
44	21.2	64.2	31	6	AX425651	AX425651 Sequence
45	21.2	64.2	31	6	AX582640	AX582640 Sequence

ALIGNMENTS

RESULT 1
BD242794
LOCUS BD242794 33 bp DNA linear PAT 17-JUL-2003
DEFINITION Catalytic molecules.
ACCESSION BD242794
VERSION BD242794.1 GI:33052564
KEYWORDS JP 2002534117-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 33)
AUTHORS Atkins,D.G., Baker,A.R. and Khachigian,L.M.
TITLE Catalytic molecules
JOURNAL Patent: JP 2002534117-A 6 15-OCT-2002;
UNISEARCH LTD,JOHNSON AND JOHNSON RESEARCH PTY LTD
COMMENT OS Artificial Sequence
PN JP 2002534117-A/6
PD 15-OCT-2002
PF 11-JAN-2000 JP 2000593730
PR 11-JAN-1999 AU PP 8103
PI DAVID G ATKINS,ANDREW R BAKER,LEVON MICHAEL KHACHIGIAN PC C12N15/09,A61K31/711,A61K48/00,A61M29/02,A61P9/08,A61P9/10, PC A61P9/12,
PC C12N9/00,C12N15/00
CC Description of Artificial Sequence: DNAzyme
FH Key Location/Qualifiers
FT source 1. .33
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .33
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 100.0%; Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCGGCCAGGCTAGCTACAACGACCTGGACGA 33
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Db          1 CCGCGGCCAGGCTAGCTACAACGACCTGGACGA 33


RESULT 2
BD242795
LOCUS       BD242795                  33 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Catalytic molecules.
ACCESSION   BD242795
VERSION     BD242795.1  GI:33052565
KEYWORDS    JP 2002534117-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Atkins,D.G., Baker,A.R. and Khachigian,L.M.
  TITLE     Catalytic molecules
  JOURNAL   Patent: JP 2002534117-A 7 15-OCT-2002;
            UNISEARCH LTD,JOHNSON AND JOHNSON RESEARCH PTY LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002534117-A/7
            PD   15-OCT-2002
            PF   11-JAN-2000 JP 2000593730
            PR   11-JAN-1999 AU      PP 8103
            PI   DAVID G ATKINS,ANDREW R BAKER,LEVON MICHAEL KHACHIGIAN PC
            C12N15/09,A61K31/711,A61K48/00,A61M29/02,A61P9/08,A61P9/10, PC
            A61P9/12,
            PC   C12N9/00,C12N15/00
            CC   Description of Artificial Sequence: DNAzyme
            FH   Key -          Location/Qualifiers
            FT   source         1. .33
            FT                  /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .33
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
ORIGIN

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  Best Local Similarity   93.8%;  Pred. No. 5.3;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCGCGGCCAGGCTAGCTACAACGACCTGGACG 32
              |||| ||||||||||||||||||||| |||||
Db          1 CCGCTGCCAGGCTAGCTACAACGACCCGGACG 32


RESULT 3
AX220896
LOCUS       AX220896                  31 bp    DNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 6338 from Patent WO0159103.
ACCESSION   AX220896
VERSION     AX220896.1  GI:15548620
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 6338 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES            Location/Qualifiers
     source         1. .31
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
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                    /note="Nucleic Acid"
ORIGIN

  Query Match           74.5%;  Score 24.6;  DB 6;  Length 31;
  Best Local Similarity   87.1%;  Pred. No. 1.8e+02;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGACG 32
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Db          1 CGCGGGCAGGCTAGCTACAACGAGGTCGACG 31


RESULT 4
AX274148
LOCUS       AX274148                  31 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 1717 from Patent WO0162911.
ACCESSION   AX274148
VERSION     AX274148.1  GI:16546887
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
  TITLE     Method and reagent for the inhibition of grid
  JOURNAL   Patent: WO 0162911-A 1717 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES            Location/Qualifiers
     source         1. .31
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                    /db_xref="taxon:32630"
                    /note="Enzymatic Nucleic Acid"
ORIGIN

  Query Match           71.5%;  Score 23.6;  DB 6;  Length 31;
  Best Local Similarity   86.7%;  Pred. No. 4.1e+02;
  Matches   26;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGAC 31
              | |||  |||||||||||||||||||| |
Db          1 CCCGGTGAGGCTAGCTACAACGACCTGGTC 30


RESULT 5
CS075086
LOCUS       CS075086                  33 bp    DNA     linear   PAT 05-MAY-2005
DEFINITION  Sequence 24 from Patent WO2005033314.
ACCESSION   CS075086
VERSION     CS075086.1  GI:63091469
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sel,S. and Renz,H.
  TITLE     Method for the production of a cell and/or tissue and/or disease
            phase specific medicament
  JOURNAL   Patent: WO 2005033314-A 24 14-APR-2005;
            Transmit Gesellschaft fuer Technologietransfer mbH (DE)
FEATURES            Location/Qualifiers
     source         1. .33
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"
ORIGIN

  Query Match           71.5%;  Score 23.6;  DB 6;  Length 33;
  Best Local Similarity   86.7%;  Pred. No. 4.1e+02;
  Matches   26;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCGCGGCCAGGCTAGCTACAACGACCTGGA 30
              ||||| ||||||||||||||||||   |||
Db          1 CCGCGTCCAGGCTAGCTACAACGAGTAGGA 30
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```
RESULT 6
CS075130
LOCUS       CS075130                  33 bp    DNA     linear   PAT 05-MAY-2005
DEFINITION  Sequence 68 from Patent WO2005033314.
ACCESSION   CS075130
VERSION     CS075130.1  GI:63091513
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sel,S. and Renz,H.
  TITLE     Method for the production of a cell and/or tissue and/or disease
            phase specific medicament
  JOURNAL   Patent: WO 2005033314-A 68 14-APR-2005;
            Transmit Gesellschaft fuer Technologietransfer mbH (DE)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             70.3%;  Score 23.2;  DB 6;  Length 33;
  Best Local Similarity   89.3%;  Pred. No. 5.8e+02;
  Matches   25;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGG 29
              ||| ||||||||||||||||||  |||
Db          2 CGCCGCCAGGCTAGCTACAACGAAGTGG 29


RESULT 7
CS075141
LOCUS       CS075141                  33 bp    DNA     linear   PAT 05-MAY-2005
DEFINITION  Sequence 79 from Patent WO2005033314.
ACCESSION   CS075141
VERSION     CS075141.1  GI:63091524
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sel,S. and Renz,H.
  TITLE     Method for the production of a cell and/or tissue and/or disease
            phase specific medicament
  JOURNAL   Patent: WO 2005033314-A 79 14-APR-2005;
            Transmit Gesellschaft fuer Technologietransfer mbH (DE)
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             70.3%;  Score 23.2;  DB 6;  Length 33;
  Best Local Similarity   89.3%;  Pred. No. 5.8e+02;
  Matches   25;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GGCCAGGCTAGCTACAACGACCTGGACG 32
              | |||||||||||||||||||| || ||
Db          5 GCCCAGGCTAGCTACAACGACCGGGGCG 32


RESULT 8
AX220857
LOCUS       AX220857                  31 bp    DNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 6299 from Patent WO0159103.
ACCESSION   AX220857
VERSION     AX220857.1  GI:15548581
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 6299 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
ORIGIN

  Query Match             69.7%;  Score 23;  DB 6;  Length 31;
  Best Local Similarity   83.9%;  Pred. No. 6.9e+02;
  Matches   26;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGACG 32
              ||| ||| ||||||||||||||||  || ||
Db          1 CGCCGCCGGGCTAGCTACAACGACGGGGCCG 31


RESULT 9
AX274253
LOCUS       AX274253                  31 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 1822 from Patent WO0162911.
ACCESSION   AX274253
VERSION     AX274253.1  GI:16546992
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
  TITLE     Method and reagent for the inhibition of grid
  JOURNAL   Patent: WO 0162911-A 1822 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Enzymatic Nucleic Acid"
ORIGIN

  Query Match             69.1%;  Score 22.8;  DB 6;  Length 31;
  Best Local Similarity   92.3%;  Pred. No. 8.1e+02;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GCCAGGCTAGCTACAACGACCTGGAC 31
              || ||||||||||||||||||| ||||
Db          5 GCTAGGCTAGCTACAACGACCAGGAC 30


RESULT 10
AX425682
LOCUS       AX425682                  31 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 4018 from Patent WO0188124.
ACCESSION   AX425682
VERSION     AX425682.1  GI:21529064
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 4018 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Enzymatic Nucleic Acid"
ORIGIN

  Query Match             69.1%;  Score 22.8;  DB 6;  Length 31;
  Best Local Similarity   92.3%;  Pred. No. 8.1e+02;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GGCCAGGCTAGCTACAACGACCTGGA 30
              |||||||||||||||||||| ||| |
Db          4 GGCCAGGCTAGCTACAACGAACTGCA 29


RESULT 11
CS075117
LOCUS       CS075117                  33 bp    DNA     linear   PAT 05-MAY-2005
DEFINITION  Sequence 55 from Patent WO2005033314.
ACCESSION   CS075117
VERSION     CS075117.1  GI:63091500
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sel,S. and Renz,H.
  TITLE     Method for the production of a cell and/or tissue and/or disease
            phase specific medicament
  JOURNAL   Patent: WO 2005033314-A 55 14-APR-2005;
            Transmit Gesellschaft fuer Technologietransfer mbH (DE)
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             69.1%;  Score 22.8;  DB 6;  Length 33;
  Best Local Similarity   92.3%;  Pred. No. 8.1e+02;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GCGGCCAGGCTAGCTACAACGACCTG 28
              |||| |||||||||||||||| |||
Db          3 GCGGTCAGGCTAGCTACAACGAGCTG 28


RESULT 12
CS075118
LOCUS       CS075118                  33 bp    DNA     linear   PAT 05-MAY-2005
DEFINITION  Sequence 56 from Patent WO2005033314.
ACCESSION   CS075118
VERSION     CS075118.1  GI:63091501
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sel,S. and Renz,H.
  TITLE     Method for the production of a cell and/or tissue and/or disease
            phase specific medicament
  JOURNAL   Patent: WO 2005033314-A 56 14-APR-2005;
            Transmit Gesellschaft fuer Technologietransfer mbH (DE)
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             69.1%;  Score 22.8;  DB 6;  Length 33;
  Best Local Similarity   92.3%;  Pred. No. 8.1e+02;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 CCAGGCTAGCTACAACGACCTGGACG 32
              |||||||||||||||||||| || ||
Db          7 CCAGGCTAGCTACAACGACCAGGGCG 32


RESULT 13
AX426000
LOCUS       AX426000                  31 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 4336 from Patent WO0188124.
ACCESSION   AX426000
VERSION     AX426000.1  GI:21529386
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 4336 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Enzymatic Nucleic Acid"
ORIGIN

  Query Match             67.9%;  Score 22.4;  DB 6;  Length 31;
  Best Local Similarity   95.8%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGCGGCCAGGCTAGCTACAACGAC 25
              ||||| ||||||||||||||||||
Db          1 CGCGGTCAGGCTAGCTACAACGAC 24


RESULT 14
CS075168
LOCUS       CS075168                  33 bp    DNA     linear   PAT 05-MAY-2005
DEFINITION  Sequence 106 from Patent WO2005033314.
ACCESSION   CS075168
VERSION     CS075168.1  GI:63091551
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sel,S. and Renz,H.
  TITLE     Method for the production of a cell and/or tissue and/or disease
            phase specific medicament
  JOURNAL   Patent: WO 2005033314-A 106 14-APR-2005;
            Transmit Gesellschaft fuer Technologietransfer mbH (DE)
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Homo sapiens"
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             67.9%;  Score 22.4;  DB 6;  Length 33;
  Best Local Similarity   81.2%;  Pred. No. 1.1e+03;
  Matches   26;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 CGCGGCCAGGCTAGCTACAACGACCTGGACGA 33
              | ||||||||||||||||||||  |  | ||
Db          2 CCCGGCCAGGCTAGCTACAACGAAGTAAATGA 33


RESULT 15
AX426030
LOCUS       AX426030                 31 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 4366 from Patent WO0188124.
ACCESSION   AX426030
VERSION     AX426030.1  GI:21529416
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 4366 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Enzymatic Nucleic Acid"
ORIGIN

  Query Match             67.3%;  Score 22.2;  DB 6;  Length 31;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+03;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GGCCAGGCTAGCTACAACGACCTGGAC 31
              || |||||||||||||||||| || ||
Db          4 GGTCAGGCTAGCTACAACGACTTGCAC 30


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